GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 34

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.		* Query Match Length DB	ength	DB	ID	Description
۳	3216		620	23	ABG61581	High growth methan
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w	3216	100.0	620	22	AAU80325	Methylomonas 16a O
4	2069.5	64.4	627	22	AAU00012	Pseudomonas aerugi
(J)	2069.5	64.4	627	23	AA021846	Isoprenoid related
σ	2063.5	64.2	627	22	AAU00014	Pseudomonas aerugi
7	2061.5	64.1	627	2	AAU00013	Pseudomonas aerugi
89	2014.5	62.6	620	22	AAU38490	Salmonella typhi c
9	2000.5	62.2	620	20	AAY52832	Escherichia coli p

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AAG42535	AAY14144	AAO21848	AAB20543	AAB20542	AAO21849	AA021851	AAY51667	AAY51612	AAY52833	AAY15157	AAY97414	AA021854	AAM48247	AAM48245	AAG42534	AAM48246	AA021855	AAY14146	AAY14145	AAY97415	AA021857	AA021858	AAY97422	AAO21856	AAY52834	AA021845	AAO21847	ABP77532	AA021861	AA021862	AAO21860	AAU34475	AAY51613	AAB20544	AAY08880
Arabidopsis thalia	a 1-d	Isoprenoid related	c	Symechocystis sp.	Isoprenoid related	Isoprenoid related	A. thaliana	A. thaliana DOXS p	Rhodobacter sphaer	Tagetes erecta put	oybean 1-dec	Isoprenoid related	~	Arabidopsis thalia	Arabidopsis thalia	Truncated deoxyxyl	Isoprenoid related	_	M. piperita 1-deox		Isoprenoid related	enoi	تن	9	. ,	Тe	Isoprenoid related		Ä	soprenoid re	Ä	۲	. coli DOXS prot	scherichia coli	. coli DXS pr

ALIGNMENTS

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Koffas M, Odom JM, Schenzle A; WPI; 2002-452200/48.	(DUPO) DU PONT DE NEMOURS & CO E I.	01-SEP-2000; 2000US-229858P.	28-AUG-2001; 2001WO-US26827.	14-MAR-2002.	WO200220728-A2.	Methylomonas 16a.	nitrous oxide; terpenoid; animal feed; carotenoid; exopolysaccharide.	methane-containing environment; waste water treatment system; isoprenoid;	ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill;	<pre>methane; methano1; Embden-Meyerhof carbon flux pathway; 16s RNA; pvrophosphate dependent phosphofritokinase: nitrogen-containing compound:</pre>	High growth methanotrophic bacterial strain; Cl carbon substrate; enzyme;	High growth methanotrophic bacterial strain polypeptide #31.	27-AUG-2002 (first entry)	ABG61581;	LT 1 1581 ABG61581 standard; Protein; 620 AA.

New high growth methanotrophic bacterial strain, useful for producing single cell proteins, grows on a Cl carbon substrate, and comprises a functional gene encoding in Embden-Meyerhof carbon pathway -

157pp; English

The invention relates to a high growth methanotrophic bacterial strain, comprises a functional Embden-Meyerhof carbon flux pathway comprising a comprises a functional Embden-Meyerhof carbon flux pathway comprising a comprise a pyrophosphate dependent phosphofrutokinase enzyme or a 16s compression and for the biotransformation of a nitrogen-containing compound, compound, nitrate, nitrite or nitrogen. It is also useful for the production of a feed product comprising a protein, carbohydrates and a compression of a protein, carbohydrates and a compression of a feed product comprising a protein, carbohydrates and a compression of a containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are containing environments such as landfills, waste the present. The bacterial strain of the invention can be used as a containing compound of a protein source. It is also used in the containing environment carbohydrates and a wide contained to grant the protein of bromass including proteins carbohydrates and a wide contained to grant the granticularly for isoprenoid pigments for the contained compounds, useful as pigments and as monomers in polyments carbohydrates and as monomers in polyments contained and contained and contained to the proteins of the invention of terpenoid and contained and in production of exopolysacharides at high levels.

Sequence 620 A.

Similarity

100.0%; 100.0%;

Score 3216; DB 23; Pred. No. 1.2e-285;

Length

В Ś 밁 Ś 밁 Ś 몺 Ś В Ś 밁 δ 밁 S 밁 Q 맒 S Query Match Best Local S Matches 620 421 421 361 361 301 301 241 241 181 181 121 121 620; 61 61 HSSTSISAALGYAIASQLRGEDKKMVAIIGDGSITGGWAYEAMNHAGDVNANLLVILNDN MKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTV ALHYVFNTEVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVG MKLTTDYPLLKNIHTPADÍRALSKDQLQQLADEVRGYLTHTVSÍSGGHFAAGLGTVELTV ALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREEL PGAAIDPTLTALBIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQ AGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQHHGPASVRYPRGKG NRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDR DMSISPPVGAMNNYLTKVLSSKPYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGT HSSTSISAALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDN <u>ALHYVFNTEVDQLVMDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESBYDAFGVG</u> AGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQHHGPASVRYPRGKG PAFDPTKDFLPKAAPSPHPTYTEVPGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFP PAFDETKDFLPKAAPSPHPTYTEVFGRWLCDMAAQDBRLLGITPAMREGSGLVEFSQKFP LFEELGFNYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGV Conservative 0 Mismatches 0 Indels 0 Gaps 540 180 60 60 480 420 360 300 300 240 180 120 120 540 480 420 360

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Similarity

100.0%; llarity 100.0%; Conservative 0

Score 3216; DB 23; Pred. No. 1.2e-285; ; Mismatches 0;

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MKLTTDYPILKNIHTÞAÐIRÁLSKÐQLQOLAÐEVRGYLTHTVSISGGHFAAGLGTVELTV

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AA 片 밁 δ RESULT encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carb substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. D-1-deoxyxyluiose-5-phosphate synthase (Dxs) Carotenoid; isopentenyl pyrophosphate; antheraxanthin; danti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; D-1-deoxyxylulose-5-phosphate synthase; Dxs. AAE22301 standard; Protein; 620 07-MAR-2002 Methylomonas 16a Methylomonas 16a sp. D-1-deoxyxylulose-5-phosphate 25-JUL-2002 The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the producing carotenoid compounds e.g. antheraxanthin and astaxanthin, using microorganisms having a mucleic acid molecule encoding enzyme the carotenoid biosynthetic pathway and which metabolize single car 01-SEP-2000; 01-SEP-2000; 04-SEP-2001; 2001WO-US27420 Sequence Claim 41; substrates (BUPO) 541 2002-351711/38. used DU PONT DE NEMOURS & LSLVGLDSKGILATIEQFCA 620 Page 109-111; 156pp; English. Picataggio 620 PC, in the 2000US-229858P. 2000US-229907P. (first AA; Cheng Q, aggio SK, g invention entry) Ó Dicosimo 8 W , BE; Koffas Z synthase (Dxs) carbon 600 ķ ij

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Novel nucleic isolated from acid molecule encoding a isoprenoid biosynthetic enzyme, Methylomonas 16a, useful for the production of isoprenoid

Claim 4; Page 66-68; 84pp; English

an isoprenoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an isoprenoid compound biosynthetic enzyme, and for the microbial production of isoprenoid compounds. The molecules of the invention are also useful for regulating isoprenoid biosynthesis in an organism and for producing recombinant organisms for producing various isoprenoid compounds. The mucleic acid is also useful for feed additive, for the production of keratenoids and their derivatives, isoprenoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 1 (ORF1) dxs (1-deoxyxylulose-5-phosphate synthas enzyme) protein of the invention, as described above. The present invention relates to a new nucleic acid molecule encoding synthase

Sequence 620 AA;

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LSLVGLDSKGILATIEQFCA
                                                                    ALVLELARTHDVFVTVEENVIAGGAGSAINFFLQAQKVLMPVCNIGLPDRFVEQGSREEL
                                                                                                                                                                                                                                   NRYFDVALAEQHAVTLAAGQACQGAKPVVALYSTFLQRGYDQLLHDVALQNLDMLFALDR
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                                                                                                                                                              AGLVGPDGPTHAGAFDYSYMRCI PNMLIMAPADENBCRQMLTTGFQHHGPASVRY ERGKG
                                                                                                                                                                              AGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENBCRQMLTTGPQHHGPASVRYPRGKG
                                                                                                                                                                                                                                                                                         PAFDPTKDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFP
                                                                                                                                                                                                                                                                                                                               LFEELGFNYFGPIDGHDVBMLVSTLENLKDLTGPVFLHVVTKXGKGYAPAEKDPLAYHGV
                                                                                                                                                                                                                                                                                                                                               LFEELGFNYFGP I DGHDVEMLVSTLENLKOLTGPVFLHVVTKXGXGYAPAEXDFLAYHGV
                                                                                                         PGAAIDPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNWRFVKPFDQ
                                                                                                                        PGAAIDPTITALEIGKAEVRHIGSRIAILAWGSMVTPAVEAGKQLGATVVNVRFVKPFDQ
                                                                                                                                                                                                                  NRYFDVATABOHAVTLAAGOACOGAKPVVATYSTFLORGYDOLIHDVALQNLDMLFALDR
                                                                                                                                                                                                                                                                         PAPDPTKDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEPSQKFP
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                                                     ALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREEL
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llarity 100.0%;
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Pred. No. 1.2e-285;
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                                                                                                                                                               CC The sequence represents Pseudomonas aeruginosa deoxyxylulose-5-phosphate CC synthase, dxs. (Ant)agonists of dxs are useful for treating an individual CC in need of enhanced or inhibited activity or expression of or CC immunological response to dxs. Dxs and the nucleic acid encoding it are CC useful as diagnostic reagents, especially in relation to diseases related CC useful as probes or primers and to synthesise full length dxs CC polynucleotides. The nucleic acid and protein are useful for diagnosing CC bacterial infections, especially by Pseudomonas aeruginosa, staging a CC disease or response of an infectious organism to drugs, and are also used in a structure based design of an (ant)agonist to dxs. The nucleic acid, CC protein and antibodies raised against it are useful for screening for CC (ant)agonists of dxs or the nucleic acid and are useful to interfere with the initial physical interaction between a pathogen and amamalian host CC responsible for sequelae of infection. These molecules are useful in CC preventing adhesion of gram positive and/or gram negative bacteria to CC wounds; to block bacterial adhesion; to block the normal progression of pathogenesis in infections initiated other than by the implantation of CC in-dwelling devices or by other surgical techniques. Dxs is also useful for irreating Helicobacter pylori infection, and also to CC carcinoma.
                                                                Matches
                                                                              Query Match
Best Local :
                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New deoxyxylulose-5-phosphate (dxs) polypeptides of Pseudomonas aeruginosa useful for diagnosis of dxs expression or activity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Huang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Decxyxylulose-5-phosphate synthase; dxs; agonist; antagonist; diagnostic, eukaryotic extracellular matrix protein; antibody; wound; in-dwelling device; Helicobacter pylori infection; gastric ulcer; gastritis; gastrointestinal carcinoma.
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                            PLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVEN 67
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BEECHAM PLC.
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Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
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Disclosure; Fig

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246pp;

English.

invention

Query Match Best Local

Sequence

627 AA;

production of the invention.

Matches

388;

Conservative

100;

Similarity

64.48;

Score 2069.5; DB 23 Pred. No. 1.7e-180; Pred. matches 117;

76 68 16 æ

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RESULT 6
AAU00014
ID AAU0
XX
AC AAU0
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DT 08-M
XX
         08-MAY-2001
                          AAU00014;
                                           AAU00014 standard;
         (first entry)
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TPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSIS PLIDRASSPAELRRIGEADLETLADELRQYLLYTVGQTGGHFGAGLGVVELTIALHYVFD PLLKNIHTPADIRALSKDQLQQLADEVRGYLFHTVS1SGGHFAAGLGTVELTVALHYVFN

> 75 67

> 16 φ

Matches 387; Query Match Best Local Sequence

Similarity

64.28; 100; Score Pred.

Conservative

Mismatches No. 6.16

Indels Length

627; 7; Gaps

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dxs sequence given in AAU00012.

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isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoO(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS) activity or decapyrenyl diphosphate synthase (DXS) activity, is useful for increasing production of CoO(10) in a cell having endogenous DDS activity. This sequence represents a protein relating to the isoprenoid
                                                                                                      LAGSHELLVTIEENAVMGGAGSAVGEFLASEGLEVPLLQLGLPDYYVEHAKPSEMLAECG
                                                                                                                                                        LARTHDVFVTVEENVLAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
                                                                                                                                                                                                            DPDLQPVEIGKGVVRRRGGRVALLVFGVQLAEAMKVAESLDATVVDMRFVKPLDEALVRE
                                                                                                                                                                                                                                        DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLB
                                                                                                                                                                                                                                                                                                                   EDGPTHAGSFDISYLRCIPGMLVMTPSDEDELRKLLTTGYLFDGPAAVRYPRGSGPNHPI
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                                                                                                                                                                                                                                                                                                                                                                                                                       VAI AEQHAVTLAAGMACEGMKPVVAI YSTFLQRAYDQLIHDVAVQHLDVLFAI DRAGLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEAPGSAPKKTGGPKYSSVFGQWLCDMAAQDARLLGITPAMKEGSDLVAFSERYPERYPD
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The sequence represents Pseudomonas aeruginosa deoxyxylulose-5-phosphate synthase, dxs, temperature sensitive mutant, ts-80. (Ant)agonists of dxs creating the distribution of the distribution of the distribution of enhanced or inhibited activity or expression of or immunological response to dxs. Dxs and the cucleic acid encoding it are useful as diagnostic reagents, especially in relation to diseases related to expression or activity of dxs. Pxagments of the nucleic acid are useful as probes or primers and to synthesise for diagnosing bacterial infections, especially by Pseudomonas carryinosa, staging a disease or response of an infectious organism to dxs. The nucleic acid are useful for sevential to used in a structure based design of an (ant)agonist to dxs. The nucleic acid, protein and antibodies raised against it are useful for screening for (ant)agonists of dxs or the nucleic acid and are useful for acreening for lant)agonists of dxs or the nucleic acid and are pathogen and a mammalian host responsible for sequelae of infection.

CC These molecules are useful in preventing adhesion of gram positive and/or gram negative bacteria to eukaryotic extracellular matrix proteins or in-dwelling devices or in wounds; to block bacterial adhesion; to block the implantation of in-dwelling devices or by other surgical contection, and also useful for identifying membrane bound or soluble receptors. The (ant)agonists are useful for treating Helicobacter pylori infection, and also to prevent, inhibit or treating Helicobacter pylori confection, and also to prevent, inhibit or treating the locater or deprived from the dra sequence is not shown in the specification but is derived from the dra sequence given in AMMOGOL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New deoxyxylulose-5-phosphate (dxs) polypeptides of Pseudomonas aeruginosa useful for diagnosis of dxs expression or activity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-1999;
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                                                                   SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
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Jiang X,
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                                                                                                                                                                            9905-0377279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Pro replaced by Ser"
   McDevitt D;
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Sequence

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CC of the nucleic acid are useful as probes or primers and to synthesise C full length das polynucleotides. The nucleic acid and protein are useful CC for diagnosing bacterial infections, especially by Pseudomonas CC aeruginosa, stagling a disease or response of an infectious organism to CC drugs, and are also used in a structure based design of an (ant) agonist to das. The nucleic acid, protein and antibodies raised against it are CC useful for screening for (ant) agonists of dax or the nucleic acid and are useful to interfere with the initial physical interaction between a CC pathogen and a mammalian host responsible for sequelae of infection. CC These molecules are useful in preventing adhesion of gram positive and/or CC gram negative bacteria to eukaryotic extracellular matrix proteins or in-dwelling devices or in wounds; to block bacterial adhesion; to block the normal progression of pathogenesis in infections initiated other than CC the implantation of in-dwelling devices or by other surgical CC infection, and also useful for identifying membrane bound or soluble receptors. The (ant) agonists are useful for treating Helicobacter pylori infection, and also to prevent, inhibit or treat gastric ulcers, CC gastritis and gastrointestinal carcinoma.

CC from the dxs sequence is not shown in the specification but is derived CC from the dxs sequence given in AAU00012.
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthase, dxs, temperature sensitive mutant, ts-32. (Ant)agonists of dare useful for treating an individual in need of enhanced or inhibited activity or expression of or immunological response to dxs. Dxs and the nucleic acid encoding it are useful as diagnostic reagents, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page - ; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New deoxyxylulose-5-phosphate (dxs) polypeptides of Pseudomonas aeruginosa useful for diagnosis of dxs expression or activity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relation to diseases related to expression or activity of dxs. Fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represents Pseudomonas aeruginosa deoxyxylulose-5-phosphate , temperature sensitive mutant, ts-32. (Ant)agonists of dxs
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밁 S 밁 S 문 Ş 문 S 밁 S 片 S 밁 S Matches Query Match Best Local : 196 188 128 AALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDNSISPP 387; 76 89 16 œ Similarity PDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQHHGPASVRYPRGKGFGAAI VALAEQHAVTLAAGMACEGMKPVVAIYSTFLQRAYDQLIHDVAVQHLDVLFAIDRAGLVG VAIAEQHAVTLAAGQACQGAKFVVAIYSTFLQRGYDQLIHDVALQNLDNLFALDRAGLVG NYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPTK TPVDQLVMDVGHQAYPHKILTGRKBRMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSIS LEAPGSAPKKTGGPKYSSVFGQWLCDMAAQDARLLGITPAMKEGSDLVAFSERYPERYFD DFLPKAAP--SPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRYFD VGGLSNYLAKILSSRTYSSMREGSKKVLSRLPGAWEIARRTEEYAKGMLVPGTLFEELGW VGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELGF AALGMAIAARLOGKERKSVAVIGDGALTAGMAFEALNHASEVDADMLVILNDNDMSISHN 195 TPDDRLVWDVGHQAYPHKILTERRELMGTLRQKNGLAAFSRRAESEYDTFGVGHSSTSIS PLIDRASSPAELRRLGEADLETLADELRQYLLYTVGQTGGHFGAGLGVVELTIALHYVFD PLIKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVFN Conservative 64.18; 100; Score 2061.5; DB 2 Pred. No. 9.3e-180; 0; Mismatches 118; 118; DB 22; Indels Length 627 7; Gaps 485 425 307 370 365 310 255 247 135 127 75 2

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RESULT 8
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibictics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The prevention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to scenen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
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23-MAY-2000;
26-MAY-2000;
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27-NOV-2000;
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B; AAS56349.
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; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
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Xu HH;
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LDAAGIBAKIKAWLA
                                                     MAAQHDALVIILBENA IMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQEEARABLG
                                                                                                           TP-LEKLPIGKGLVKRHGEKLAILNFGTLMPEAAKVAEALNATLVDWRFVKPLDDTLILE
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                                                                                LARTHDVFVTVBENVIAGGAGSALNTFLQAQKVLMPVCNIGLPDRFVBQGSREELLSLVG
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                         LDSKGILATIEQFCA
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Pred. No. 1.9e-175;
06; Mismatches 131;
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AAY52832 standard; Protein; 620 Š

AAY52832;

26-JAN-2000 (first entry)

Escherichia co11 protein sequence SEQ Ħ NO:1.

RESULT 9
AAYS2832
ID AAYS2832
ID AAYS6
AC AAY5
AC AAY5
XX AC AAY5
XX BSch
XX Heal
XX Heal
XX Isop
XX Isop Isoprenoid; microorganism; detection; antibacterial; herbicide; heart disease; osteoporosis; haemostasis; cancer; immunopotentiation; health food; antifouling coating; farnesyl pyrolinic acid; pyruvic acideoxy-D-xylulose-5-phosphate; glycerylaldehyde-3-phosphate; 2-C-methyl-D-erythreitol-4-phosphate. acid

Escherichia coli

WO9953071-A1

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Best Local S
Matches 370
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05~AUG-1998;
15~FEB-1999;
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N-PSDB; AAZ33157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparation of recombinant isoprenoid compounds useful for treatment heart diseases, osteoporosis and hemostatis, preventing cancer and
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                                                                                                                            SAGIGIAVAAEKEGKNERTVCVIGDGAITAGMAFEAMNHAGDIEPDMLVILNDNEMSISE
                                                                                                                                                           SAALGWALASQLRGEDKKWVAIIGDGSITGGMAYEAWNHAGDVNANLLVILNDNDMSISP
                                                                                                                                                                                                                   NTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI
FNYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPT
                                                                             PVGAMMNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELG
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98JP-0221910.
99JP-0035739.
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                                                                                                                                            DPTLTALEIGKAEVRHHGSRIAILAMGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                                                                        LARTHDVFVTVEENVIAGGAGSAIWTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
                                                                                                                                                                                                                                                                      ATAEQHAVTLAAGQACQGAKEVVAIYSTELQRGYDQLIHDVALQNLDMLFALDRAGLVGF
LDAAGMEAKIKAWLA
                                                            MAASHEALVIVEENAIMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQEENRAELG
                                                                                                                                                                                   DGQTHQGAFDLSYLRCIPEMVIMTPSDENECROMLYTGYHYNDGPSAVRYPRGNAVGVEL
                                                                                                                                                                                                     DGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQHH-GPASVRYPRGKGPGAAI
                                                                                                                                                                                                                                              ATABQHAVTFAAGLAIGGYKPIVATYSTFLQRAYDQVLHDVAIQKLPVLFAIDRAGIVGA
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                             LDSKGILATIEQFCA
                                                                                                                        TP-LEKLPIGKGIVKRRGEKLAILNFGTLMPEAAKVAESLNATLVDMRFVKPLDEALILE
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AAY08880 standard; protein; 620 B

DXS protein

13-AUG-1999 AAYO8880;

(first

1-deoxy-D-xylose-5-phosphate synthase; DXS; modulator; pyruvate; glyceraldehyde-3-phosphate; GA3P; 1-deoxy-D-xylulose-5-phosphate; DXP structural analogue; pesticide; antibacterial; herbicide; biosynthesi: growth promoter; DXP derivative; isoprenoid; carotenoid; chlorophyll; phytol; lutein; sterol; ubquinone; rubber; taxane

Escherichia coli.

DE29800547-U1

08-APR-1999

16-JAN-1998; 98DB-2000547

28-NOV-1997; 97DB-1052700

(KERJ) PORSCHUNGSZENTRUM JUELICH GMBH HOECHST-SCHERING AGREVO GMBH.

1999-230818/20

1-Deoxy-D-xylulose-5-phosphate synthase protein potentially useful as pesticides, antibacterial and modulators agents, herbici herbicides

Claim ω -, Page 10; 21pp; German

ARYSULT 10
ARYOB 880
JID BAYOB 880
AXX AAYOB
AC This invention describes a 1-deoxy-D-xylulose-5-phosphate synthase (DXS) protein or active fragment and a DXS modulator. The DXS modulator is a structural analogue of pyruvate, glyceraldehyde-3-phosphate (GAB) or 1-deoxy-D-xylulose-5-phosphate (DXP). Compounds that inhibit DXS activity are potentially useful as pesticides, antibacterial agents or herbicides. Compounds that stimulate DXS activity are potentially useful as growth promoters or for increasing biosynthesis of DXP derivatives, especially isoprenoids such as carotenoids, chiorophyll, phytols, lutein, sterols, ubquinone, rubber and taxanes.

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RESULT 11

AAB20544

ID AAB20

XX AAB20

AC AAB20

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prenoid expression; 1-deoxy-D-xylulose-5-phosphate synthase; DXPS;
synthase; antibacterial; herbicide; transgenic plant.
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Best Local Similarity 60.2%;
Matches 370; Conservative 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoprenoid activity or expression modulators are used as medicaments treat bacterial diseases, and as herbicides. The method can be used to produce transgenic plants which have higher levels of isoprenoids, an which have health care benefits when consumed. The present sequence represents the DXPS protein from Bscherichia coli, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for manipulating isoprenoid expression in cells or organisms having a mevalonate independent isopentyl diphosphate (IPP) synthesising pathway. The method compriss altering the activity of 1-deoxy-D-xylulose-5-phosphate synthase (DX or a functional equivalent, derivative, or bioprecursor of it. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manipulating isoprenoid expression in cells or organisms and identifying modulators of the expression, for use in antibacterials inherbicides and to produce transgenic plants with improved properties
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Best Local S
Matches 370
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01-OCT-1998;
01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the novel use of a DNA sequence encoding 1-deoxy-D-xylulose-5-phosphate synthase (DoXS), and optionally p-hydroxyphenylbyruvate dioxygenase (HPPD) and/or geranylgeranyl-tocopherol, vitamin K, chlorophyll and/or carotenoid content. Transgenic plants containing DOXS DNA coding sequences can be used for production of plant and bacterial DOXS which also have increased tocopherol, vitamin K, chlorophyll and/or carotenoid content. The test system can be used to identify inhibitors of DOXS. This sequence represents the Escherichia coli DOXS protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOXS; 1-deoxy-D-xylulose-5-phosphate synthase; HPPD; GGPPOR; plant; p-hydroxyphenylpyruvate dioxygenase; tocopherol; vitamin K; chlorophyll; geranylgeranyl-pyrophosphate oxidoreductase; carotenoid; transgenic; ss.
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                             SAALGMAIASQLRGEDKKXVAIIGDGSITGGXAYEAMNHAGDVNANLLVILNDNDMSISP
                                                                                          NTPFDQLIWDVGHQAYPHKILTGRRDKIGTIRQKGGLHPFPWRGESEYDVLSVGHSSTSI
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       SAGIGIAVAAEKEGKNRTVCVIGDGAITAGMAFEAMNHAGDIRPDMLVILNDNEMSISE
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New polymucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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27-NCV-2000; 2000US-25362SP.
22-DEC-2000; 2000US-253693P.
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CC Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic conformat directly from MIPO at CC format directly from MIPO at the format directly f
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                                                                                                                    LARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
                                                                                                                                                                               TP-LEKLPIGKGIVKRRGEXLAILNEGTLMPEAAKVAESLNATLVDMRFVKPLDEALILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGALNNHLAQLISGKLYSSLREGGKKVFSGVPPIKELLKRTEEHIKGMVVPGTLFEBIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAALGMAIASQLRGEDKKMVAIIGDGSITGGKAYEAMNHAGDVNANLLVILNDNDMSISP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTPVDQLVWDVGHQAYPHKILTGRXERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI 126
LDAAGMEAK I KAWLA
                                                                                                                                                                                                                           DPTLTALBIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                                                                                                                                                                                                                                                      DGQTHQGAFDLSYLRCIPEMVINTPSDENECROMLYTGYHYNDGPSAVRYPRGNAVGVEL:
                                                                                                                                                                                                                                                                                                             DGPTHAGAPDYSYMRCIPNMLIMAPADENECROMLTTGFOHH-GPASVRYPRGKGPGAAI
                                                                                                                                                                                                                                                                                                                                                                AIAEQHAVTFAAGLAIGGYKPIVAIYSTFLQRAYDQVLHDVAIQKLPVLFAIDRAGIVGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDFLPKAAPSPHETYTEVEGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRYFDV
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                                         LDSKGILATIEQFCA
                                                                                          MAASHBALVTVEENAIMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQEEMRABLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNYIGPVDGHDVLGLITTLKNMRDLKGPQFLHIMTKKGRGYEPAEKDPITFHAVPKFDPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                   NTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAPPARDESEYDAFGVGHSSTSI 126
                                                                                                                                                                                                                                                                                 YPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVF
                                                                   NVGALNNHLAQLLSGKLYSSLREGGKKVFSGVPPIKELLKRTEEHIKGMVVPGTLFEELG
                                                                                   PVGAMMNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELG
                                                                                                                              SAGIGIAVAAEKEGKNRRTVCVIGDGAITAGMAFEAMMHAGDIRPDMLVILNDNEMSISE
                                                                                                                                                                                                NTPFDQLIWDVGHQAYPHKILTGRRDKIGTIRQKGGLHPFPWRGESEYDVLSVGHSSTSI
                                                                                                                                                                                                                                                                YPTLALVDSTQELRLLPKESLPKLCDELRRYLLDSVSRSSGHFASGLGTVELTVALHYVY
FNYIGPVDGHDVLGLITTLKNMRDLKGPQFLHIMTKKGRGYEPAEKDPITFHAVPKFDPS
                                                                                                                                                               SAALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISP 186
                                FWYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jessen H,
                                                                                                                                                                                                                                                                                                                                                                                              620 AA;
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                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                            62.2%;
                                                                                                                                                                                                                                                                                                                              114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
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                                                                                                                                                                                                                                                                                                                                              Score 2000.5; DB 23; Pred. No. 3.6e-174;
                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                              128;
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RESULT 15
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XX Haemo
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                                                                                         The invention relates to methods and materials for the production of isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DMS) activity, is useful for increasing production of CoQ(10) in a cell having endogenous DDS activity. This sequence represents a protein relating to the isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                    production of the
                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 6; 246pp;
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                        VGLDSKGILATIEQFCA
                                                                  LELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSL
                                                 NULAQTHDYLVTLEENAIQGGAGSAVAEVLNSSGKSTALLOLGLPDYFIPQATQQEALAD
                                                                                                                                                                                                                                                                                                       ELGFNYTGGPIDGHDVEMLVSTLENLKDLTGFVFLHVVTKKGKGYAPAEKDPLAYHGVPAF
LGLDTKGIEEKILNFIA
                                                                                                   KLTP-LEMEPIGKSRLIRKGQKIAILNFGTLLPSALELSEKLNATVVDMRFVKPIDIEMI
                                                                                                                 VGPDGPTHAGAFDYSYMRCIENMLIMAPADENBCRQMLTTGFQHHGPASVRYPRGKGPGA
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Pred. No. 2.2e-168;
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12 US-09-815-242-10068
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Sequence 2, Appli
Sequence 6, Appli
Sequence 13998, A
Sequence 13998, A
Sequence 14083, A
Sequence 14083, A
Sequence 21174, A
Sequence 21174, A
Sequence 31, Appl
Sequence 31, Appl
Sequence 15911, A
Sequence 16281, A
Sequence 15291, A
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ALIGNMENTS

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PRIOR FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOPTWARE: Microsoft Office 97
SET D NO 2
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US-09-934-903-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Koffas, I
APPLICANT: Odom, J
APPLICANT: Schenzl
APPLICANT: No. US2
APPLICANT: Tomb, J
                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: CL1646 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
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                                                                                                                                                                                             TYPE: PRT
ORGANISM: Methylomonas 16a
FEATURE:
                                                                                                                                                                                                                                                          LENGTH:
                                                                           Y Match 100.0%; Score 3216; DB 10; Local Similarity 100.0%; Pred. No. 1.1e-298; les 620; Conservative 0; Mismatches 0;
                         1 MKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVBLTV
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MKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVBLTV
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Schenzle, Andreas J.
No. US20020102690Alton,
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61 ALHYVENTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVG

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Sequence 62, Application US/09934868

Patent No. US20020137190A1

GENERAL INFORMATION:

APPLICANT: Koffas, Mattheos

APPLICANT: Codom, James M

APPLICANT: Schenzle, Andreas J

TITLO GINVENTION: DENITHIFYING METHANOTROPHIC BACTERIAL STRAIN

PILE REFERENCE: CLL596 US NA

CURRENT APPLICATION NUMBER: US/09/934,868

CURRENT APPLICATION NUMBER: 60/229,858

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Microsoft Office 97

SEQ ID NO 62

TYPE: DET
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US-09-934-868-62
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                                                                                                              Matches
                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                       OTHER INFORMATION: Amino acid sequences encoded
                                                                                                                                                                                                                         ORGANISM: Methylomonas 16a FEATURE:
                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                              Local Similarity
nes 620; Conser
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ALHYVFNTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVG 120
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                                     MKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHPAAGLGTVELTV
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APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Odom, J. Martin
APPLICANT: Picataggio, Steve
APPLICANT: Picataggio, Steve
APPLICANT: ROUVIER. Pierre E.
FILE REFERENCE: CL1903 US NA
CURRENT PILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
SOPTWARE: Microsoft Office 97
SEQ ID NOS: 60
SOPTWARE: Microsoft Office 97
SEQ ID NOS: 60
TRUGTH: 620
                                                                                         LENGTH: 620
TYPE: PRT
ORGANISM: Methylomonas
US-09-941-947A-6
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US-09-941-947A-6
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             Query Match
Best Local Similarity
Matches 620; Conserv
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APPLICANT:
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DiCosimo, Deana J.
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             100.0%; Score 3216; DB 11; illarity 100.0%; Pred. No. 1.1e-298; Conservative 0; Mismatches 0;
                                                                                                          16a
                 Indels
                                                   Length 620;
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600

540

480

420

360

300

420

240

240

0

Gaps

0;

195

135

127 75

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RESULT 4
US-10-369-493-13998
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                                                                                                                       SEQ ID NO 13998
LENGTH: 628
Query Match 64.7
Best Local Similarity 63.2
Matches 387; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13998, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)8

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR PILING DATE: 2002-02-21

NUMBER OF SEQ. ID NOS: 47374
                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                    TYPE: PRT
ORGANISM: Pseudomonas
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64.7%; Score 2080; DB 1
63.2%; Pred. No. 7e-190;
tive 101; Mismatches 12
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                                DB 12;
   120;
   Indels
                                  Length
                                    628;
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                                                                                                                            APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PC/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-10-381-779-15
; Sequence 15, Application US/10381779
; Publication No. US20030219798A1
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Query Match 64.4%; Score 2069.5; Best Local Similarity 63.4%; Pred. No. 7.1e Matches 388; Conservative 100; Mismatches
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gokarn, Ravi R
                                                                                  LENGTH: 627
TYPE: PRT
ORGANISM: Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDEVGIEAAVRE 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---APAÅAPKKAGGPKYSGVPGEWLCDMÅAADPRLVGITPAMKEGSDLVAPSERFPLRYFD 373
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                                                                                      aeruginosa
 .1e-189;
es 117;
                                  DB 12;
                                  Length
                                    627;
 7;
Gaps
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553 545 493 433

365 315

613 509

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RESULT 6
US-09-815-242-14083
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                                                                                                      CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR ENTITION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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APPLICANT:
APPLICANT:
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Yamamoto, Robert T.
Xu, H. Howard
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RESULT 7
US-10-369-493-481
; Sequence 481, Applicat.
; Publication No. US200302336...
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
rttle OP INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANT OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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LEWCTH: 620
; TYPE: PRT
; ORCANISM: Salmonella typhi
US-09-815-242-14083
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
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Pred. No. 1.3e-183;
6; Mismatches 131;
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RESULT 8
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CURRENT ETLING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 481
LENGTH: 619
TYPER: TOTAL
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; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-481
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61.8%; Pred. No. 1.2e-182;
Live 102; Mismatches 129; II
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; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21174
; LENGTH: 620
; TYPE: PRT
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US-09-815-242-10068
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                                                                                                                                          Sequence 10068, Application US/09815242
Patent No. US2002061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
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Best Local Similarity
Matches 377; Conserv
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                                                                         Carr, Grant J.
Yamamoto, Robert
                                                                                                                 Trawick, John D.
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10068
LENGTH: 620
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Best Local :
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ORGANISM: Escherichia
-09-815-242-10068
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LDSKGILATIEQFCA 620
                                      HAASHEALVIVEENAIMGGAGSGVNEVLMAHKKVVVVLNIGLFDFFIPQGTQEEMKAELG
                                                                          LARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
                                                                                                                                                DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNWRFVKPFDQALVLE
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Pred. No. 2.8e-182;
4; Mismatches 128;
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
ITILE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR APPLICATION UNMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 620
TYPE: PRT
ORGANISM: Escherichia coli
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US-10-381-779-31
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Publication No.
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                                                                                                                                                                                                            DGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFOHH-GPASVRYPRGKGFGAAI
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LDAAGMEAKIKAWLA
                                        MAASHEALVTVEENAIMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQEEMRAELG
                                                                            LARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
                                                                                                                TP-LEXLPIGXGIVKRRGEKLAILNFGTLMPEAAKVAESLNATLVDMRFVKPLDEALILE
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No. US20030219798A1
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Pred. No. 2.8e-182;
14; Mismatches 128; I
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Length 620;

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-2B
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-2B
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 731
LENGTH: 620
TYPE: PRT
TYPE: PRT
CRANISM: Escherichia coli
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                                    TP-LEXLPIGKGIVKRRGEKLAILNFGTLMPBAAKVAESLNATLVDMRFVKPLDBALILE
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LDSKGILATIEQFCA
                                                                                                                                           DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNWRFVKPFDQALVLE 545
                                                                                                                                                                                                          DGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFOHH-GPASVRYPRGKGPGAAI 485
                                                                                                                                                                                                                                                      AIABQHAVTFAAGLAIGGYKPIVAIYSTFLQRAYDQVLHDVAIQKLPVLFAIDRAGIVGA
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o. US20030233675A1
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2.8e-182;
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US-10-369-493-15911
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15911
LENGTH: 623
TYPE: PRT
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Grey
APPLICANT: Slater, Ste
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Publication No. US20030233675A1
GENERAL INFORMATION:
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                       GPGAAIDPTLTALBIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFD
                                                                                                                                                                                                  RAGIVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMITIGFQHHGPASVRYPRGK 479
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   LLSLVGLDSKGILATI
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Pred. No. 1.7e-181;
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US-10-369-493-16281
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16281
LENGTH: 623
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                                                                                                       QALVIBIARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREE 599
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LLSLVGLDSKGILATI 615
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US-10-369-493-15540
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15540
LENGTH: 653
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Best Local .
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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APPLICANT: Hinkle, Gre
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FEATURE:
WAME/KEY: unsure
LOCATION: (1)..(653)
OTHER INFORMATION: unsure at all
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Similarity 61.4%;
QALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREE
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                                                     GPGTALDASLTTLPIGKAQLRHSGARIALLGFGATVDAAEAVGRELGLTVVNMRFVKPLD
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTBINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7428
LENGTH: 619
TYPE: PRT
ORGANISM: Burkholderia cepacia
US-10-369-493-7428
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US-10-369-493-7428
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Publication No. US20030233675A1
538 FDQALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSR 597
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                                                VATIKQMTALPLGKGEIRRETSQPAGKRIAILAFGTMVAPSLAAAEQLDATVANMRFVKP 541
                                                                          AAIDPTUTALEIGKAEVRHH-----GSRIAILAWGSWYTPAVEAGKQLGATVVNMRFVKP 537
                                                                                                                                           UGADGATHAGAYDLAFLRCIPNMTVMAASDENECROMLYTALQQPNPTAVRYPRGAGTG
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US-09-146-221-6
US-09-626-589-2
US-09-626-589-3
US-09-626-589-3
US-09-626-589-3
US-09-626-589-3
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US-09-146-221-4
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ALIGNMENTS

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323 LEAPGSAPKKTGGPKYSSVFGQWLCDMAAQDARLLGITPAMKEGSDLVAFSERYPERYFD 382	WLCDMAAQDERLLGITPAMREGSGLVEFS		248 NYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDFTK 307		HALLOTTA LAWKLOGSKEKKS VAV LUDGALT AGMAT BALINHAS SVUADMEV LLINDNUMS I SHN	AALGMAIASQIRGEDKKWVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISPP	LTERRELMGTLROKO	68 TPVDQLVMDVGHQAYPHKILTGRXERMPTIRTLGGVSAFPARDESSYDAFGVGHSSTSIS 127	28 PILDRASSPABLRRIGBADLETLADELRQYLLYTVGQTGGHFGAGLGVVELTIALHYVFD 87	RALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELT	/ Match 64.4%; Score 2069.5; DB 4; Length 639; Local Similarity 63.4%; Pred. No. 4e-199; hes 388; Conservative 100; Mismatches 117; Indels 7; Gaps 2;	RESULT 1 US-09-252-991A-26388 Sequence 26388, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: MATC J. Rubenfield et al. APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107195.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 26388 LENGTH: 639 TYPE: PRT ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26388

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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING '
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6210
LENGTH: 648
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Best Local Similarity
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Patent No. 6562951
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----SGGKTP-PKYSDVFGEWLCDBAAQDERLLAITPAMCBGSGMVKFAKQFPQRFFDVA 378
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TITLE OF INVENTION: Plant 1-Deoxy-Xylulose 5-1
FILE REFERENCE: BB1290
CURRENT APPLICATION UNMER: US/09/857,556A
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,779
PRIOR FILING DATE: 1998-12-03
NUMBER OF SRQ ID NOS: 34
SOFTWARE: Microsoft Office 97
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LENGTH: 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.2%; Score 1485.5; DB 4
Best Local Similarity 49.2%; Pred. No. 2.8e-140;
Matches 314; Conservative 102; Mismatches 185;
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APPLICANT:
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TYPE: PRT
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 412 LDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENE-CRQMLTTGFQHHGP 470
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                                                          LNYFLRRFPNRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFLQRGYDQVVHDVDLQK 487
                                                                                                                                                                     PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG
                                                                                                                                                                                                                                          ~VPGTLFEBLGFNYFGPIDGHDVEMLVSTLENLKD~~LTGFVFLHVVTKKGKGYAPAEKD 293
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                                                                               LVBFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
                                                                                                                                ADKYHGVAKFDPATGKQF---KSPAKTLSYTNYFABALIAEAEQDNRVVAIHAAMGGGTG
                                                                                                                                                                                                        GSGSTLFEELGLYYIGPVDGHNIDDLITILREVKSTKTTGPVLIHVVTEKGRGYPYAERA
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APPLICANT: Zude Weng
APPLICANT: APPLICANT: Mark E. Williams
FILE REFERENCE: BB1290
CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,779
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 34
SOFTMARE: Microsoft Office 97
SEQ ID NO 34
LENGTH: 594
TYPE: PRT
ORGANISM: Oryza sativa
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US-09-857-556A-34
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Patent No. 6558915
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APPLICANT: Sean J. Coughlan
APPLICANT: Yong Tao
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  RAGIVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENE-CROMLTTGFQHHGPASVRYPRG 478
                                                                                                                                                                              AFDPT -- KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKF 359
                                                                                                                                                                                                                                           BIGFNYFGPIDGEDVEMLVSTLENLKD--LTGPVFLHVVTKKGKGYAPABKDPLAYHGVP 301
                                                                                                                                                                                                                                                                                                                                    PVGAMNNYLTKVLSSKFYSSVRBESKKALAKM-PSVWELARKTBEHVKGMI--VPGTLFE 243
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RDLKGGKNNVVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTATLDGPAP 182
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                                                             PNRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFLQRGYDQVVHDVDLQKLPVRFAMD
                                                                                                                                        KÉDPATGKOF---KSPAKTLSYTNYFAEALIAEAEQDNRVVAIHAAMGGGTGLNYFLRRF
                                                                                                                                                                                                                      BLGLYYIGPVDGHNIDDLITILREVKSTKTTGPVLIHVVTEKGRGYPYABRAADKYHGVA
                                                                                                                                                                                                                                                                                                    PVGALSSALSKLOSSRPLREIREVAKGVTKQIGGSVHELAAKVDEYARGMISGSGSTLFE 242
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                                                                                              PURYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQULDMLFALD
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US-09-857-556A-12
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PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 708
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APPLICANT: Mark E. Williams
ITILE OF INVENTION: Plant 1-Deoxy-Xylulose 5-Phosphate Synthase
FILS REFERENCE: BB1290
CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT FILING DATE: 2001-06-04
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ASVRYPRGKGPGAAIDFT---LTALEIGKAEVRHHGSRIAILAWGSMYTPAVEAGK----
                                                                                                                                                                              LVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
                                                             LPVRFAMDRAGEVGADGPTHCGSPDVTFMACLPNMVVMAPSDEADLFHMVATAAAINDRP
                                                                                  LDMLFALDRAGLVGPDGPTHAGAPDYSYMRCIPNWLIMAPADENECROMLTTGPQ-HHGP 470
                                                                                                                                        MNLFHRRFPTRCEDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFMQRAYDQVVHDVDLQK 479
                                                                                                                                                                                                                    ADKYHGVTKFDPPTGKQFKSKATTQSYTTY---FAEALIAEAEADKDVVAIHAAMGGGTG
                                                                                                                                                                                                                                                          PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG
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                                                                                                                                                                                                                                                                                                                             -VPGTLFEELGFNYFGFIDGHDVEMLVSTLENLKD--LIGFVFLHVVTKKGKGYAPAEKD 293
                                                                                                                                                                                                                                                                                                                                                                              ATEDGPTPPVGALSSALSRLQSNRPLRELREVAKGVTKRIGGPMHELAAKVDEYARGMIS 302
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APPLICANT: Croceau, Rodney B
APPLICANT: Lange, Bernd M
APPLICANT: Lange, Bernd M
APPLICANT: Wildung, Mark R
APPLICANT: McCaskill, David G
ITILE OF INVENTION: Nucleic and Amino Acid Sequences Relating to a No. 619089:
ITILE OF INVENTION: Transketolase, and Methods for the Expression Thereof
FILE REFERENCE: No. 6190895el transketolase from peppermint
CURRENT APPLICATION NUMBER: US/09/146,221
CURRENT APPLICATION NUMBER: 60/056,033
EARLIER APPLICATION NUMBER: 60/056,033
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 724
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US-09-146-221-6
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US-09-146-221-6
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Best Local S
Matches 298
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VRYPRGKGPGAAIDPTL--TALEIGKAEVRHHGSRIAILAWGSMYTPAVEAGKQL-----
                                                                                        MLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROML-TTGFOHHGPAS
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                                                                                                                                              I FOKOFPDRCFDVGIAEOHAVTFAAGMAAEGLKPFCAIYSSFLORGYDQVVHDVDLOKLP
                                                                                                                                                                                  EFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLD 413
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46.9%; Pred. No. 1.6e
tive 116; Mismatches
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LENGTH: 72
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CURRENT FILLNG DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 60/056,033
EARLIER FILLNG DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 12
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APPLICANT: Lange, Bernd M
APPLICANT: Lange, Bernd M
APPLICANT: Wildung, Mark R
APPLICANT: McCaskill, David G
TITLE OF INVENTION: Nucleic and Amino Acid Sequences Relating to a No. 6190895el
TITLE OF INVENTION: Transketolase, and Methods for the Expression Thereof
FILE REPERENCE: No. 6190895el transketolase from peppermint
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                                                              VRÉMINDRAGVVGADGETHCGAEDITYMACLENIMVVMAESDEAELMIMIATAAI IDDRESC
                                                                                   MLFALDRAGLVGPDGFTHAGAFDYSYMRCIPNMLIMAPADENECRQML-TTGFQHHGPAS
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46.8%; Pred. No. 1.6e-133;
tive 116; Mismatches 190;
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lanning, Beth
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: INDENTIFICATION OF MODULATORS OF DECXYXYLULOSE 5-PHOSPHATE
TITLE OF INVENTION: SYNTHASE ACTIVITY
FILE REFERENCE: 2037 US
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CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 6
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 ASVRYPRGKGPGAAIDP--TLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAG-----K
                                                          LPVRFAMDRAGLVGADGFTHCGAFDVTFMACLFNMIVMAPSDEADLFNMVATAVAIDDRP
                                                                                    LDMLFALDRAGIVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQ-HHGP 470
                                                                                                                              LNLFQRRFPTRCFDVGIAEQHAVTFAAGLACEGEKPFCAIYSSEMQRAYDQVVHDVDLQX
                                                                                                                                                                  LVBFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
                                                                                                                                                                                                                                          PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPVDQLVWDVGHQAYPHKILIGRKERWPTIRTLGGVSAFPARDESEYDAFGVGHSSTSIS 127
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Kloti, Andreas
Crawford, John
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                                                                                                                                                                                                         DDKYHGVVKFDPATGRQF---KTINKTQSYTTYFABALVABAEVDKDVVAIHAAMGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPQDKILWDVGHQSYPHKILTGRRGKMPTMRQTNGLSGFTKRGESEHDCFGTGHSSTTIS 136
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46.6%; Pred. No. 6.8e-133;
tive 115; Mismatches 188;
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; ORGANISM: Arabidopsis thaliana
US-09-626-589-1
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APPLICANT: Crawford, John
APPLICANT: Crawford, John
APPLICANT: Crawford, John
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF DEOXYXYLULOSE 5-PHOSPHATE
TITLE OF INVENTION: SYNTHASE ACTIVITY
FILE REFERENCE: 2037 US
CURRENT APPLICATION NUMBER: US/09/626,589
CURRENT APPLICATION NUMBER: US/09-626,589
CURRENT APPLICATION HOMBER: 2000-077-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 717
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Best Local Similarity
Matches 297; Conserv
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Patent No. 6326164
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471 ASVRYPRGKGPGAAIDP--TLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAG----
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                                                      LPVRFAMDRAGLVGADGPTHCGAFDVTFMACLPNMIVMAPSDEADLFNMVATAVAIDDRP
                                                                                         LDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQ-HHGP 470
                                                                                                                                                                LVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
                                                                                                                                                                                                     DDKYHGVVKFDPATGRQF---KTTNKTQSYTTYFAEALVAEAEVDKDVVAIHAAMGGGTG
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                                                                                                                              LNLFQRRFFTRCFDVGIAEQHAVTFAAGLACEGLKFFCAIYSSFMQRAYDQVVHDVDLQK
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APPLICANT: Rice, John
APPLICANT: Kloti, Andreas
APPLICANT: Crawford, John
APPLICANT: Lanning, Beth
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: SYMTHASE AND COMPOSITIONS FOR THE
TITLE OF INVENTION: INDENTIFICATION OF MODULATORS OF DEOXYXYLULOSE 5-PHOSPHATE
TITLE OF INVENTION: SYMTHASE ACTIVITY
FILE REFERENCE: 2037 US
CURRENT APPLICATION NUMBER: US/09/626,589
CURRENT APPLICATION NUMBER: US/09/626,589
CURRENT FILING DATE: 200-07-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version ' '
SEQ ID NO 3
SEQ ID NO 3
LENGTH: B24
TYPE: PPT
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OTHER INFORMATION: FOTHER INFORMATION
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ORGANISM: Artificial Sequence
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      LDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQ-HHGP
                                                                                                                      LVEFSQKFPNRYFDVALAEQHAVTLAAGQACQGAKPVVALYSTFLQRGYDQLIHDVALQN 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDN-DMSI-- 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGLGMAVGRDLKGKONNVVAVIGDGAMTAGQAYEAMONAGYLDSDKIVILNDNKQVSLPT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPQDKILWDVGHQSYPHKILTGRRGKMPTMRQTNGLSGFTKRGESEHDCFGTGHSSTTIS 301
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US-09-857-556A-10
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LENGTH: 721
TYPE: PRT
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Matches
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Patent No. 6558915
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APPLICANT: Mark E. Williams
TITLE OF INVENTION: Plant 1-Deoxy-Xylulose 5-Phosphate Synthase
FILE REFERENCE: BRI290
CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT FILING DATE: 2001-06-04
CURRENT FILING DATE: 60/110,779
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PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AALGMAIASQLRGEDKKMVAIIGDGSIIGGMAYEAMNHAGDVNANLLVILNDN-DMSIS- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 APKDKILWDVGHQSYPHKILTGRRDKWHTWRQTDGLAGFTKRSESDYDCFGTGHSSTTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302;
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LDMLFALDRAGLYGPDGPTHÄGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQ-HHGP
                                                                                                                                                                                                                                                                                                              GSGSTLFEELGLYYIGFVDGHNIDDLVSILNEVKSTKTTGFVLLHVVTEKGHGYPYAERA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                    ANIDGPIPEVGALSSALSKIQSNRPIRELREVAKGVTKQIGGPMHELAAKVDEYARGMIS
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                                                                                                                      LVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
                                                                                                                                                                                 ADKYHGVTKFDPATGKQFKSNÄÄTQSYTTY---FAEALIAEAEADKDIVGIHAANGGGTG
                                                                                                                                                                                                                                            PLAYHGVPAFDPT--KDFLPKAAPSPHFTYTEVFGRWLCDMAAQDERLLGITPAMREGSG
                                                                                                                                                                                                                                                                                                                                                                   -VPGTLEEELGENYFGPIDGHDVBMLVSTLENLKD--LTGPVFLHVVTKKGKGYAPAEKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PPVGAMNNYLTKVLSSKFYSSVREESKKALAKMPS-VWELARKTEEHVKGMI-
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47.0%; Pred. No. 1e-132;
tive 107; Mismatches 18
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CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,779
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 3
LENGTH: 719
TYPE: PRI
ORGANISM: Capsicum annuum
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Best Local (
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Patent No. 6558915
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APPLICANT: Mark E. Williams
TITLE OF INVENTION: Plant 1-Deoxy-Xylulose 5-Phosphate Synthase
FILE REFERENCE: BB1290
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                                                                                                                                                              PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG
                                                                                                                                                                                                      GSGSTLFEELGLYYIGPUDGHNIDDLISILKEVRSTKTTGPVLIHVVTEKGRGYPYAERA 373
  {\tt LDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQ-HHGP}
                                          MNLFLRRFPTRCFDVGIAEOHAVTFAAGLACEGLKPFCAIYSSFMORAYDOVVHDVDLQK
                                                                               LVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN
                                                                                                                         ADKYHGVAKFDPATGKQFKGSAKTQSYTTY---FABALIABABADKDIVAIHAAMGGGTG
                                                                                                                                                                                                                                  -VPGTLFEELGFNYFGPIDGHDVEMLVSTLENLKD--LTGPVFLHVVTKKKGKGYAPAEKD 293
                                                                                                                                                                                                                                                                                   ATLDGPVPPVGALSSALSRLQSNRPLRELREVAKGVTKQIGGPMHELAAKVDEYARGMIS
                                                                                                                                                                                                                                                                                                                                                                                                       AALGMAIASQLRGEDKKWVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDN-DMSIS- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVFN 67
                                                                                                                                                                                                                                                                                                                     -----PPVGAMNNYLTKVLSSKFYSSVREBSKKALAKMPS-VWELARKTEEHVKGMI-
                                                                                                                                                                                                                                                                                                                                                                  AGLGMAVGRDLKGRNNNVIAVIGDGAMTAGQAYBAMNNAGYLDSDMIVILNDNRQVSLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSIS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIVDTINYPIHMKNISLKELKQLADELRSDTIFNVSKTGGHLGSSLGVVBLTVALHYVFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114; Mismatches 193; Indels
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; ORGANISM: Mentha piperita
US-09-146-221-4
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 721
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Best Local
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APPLICANT: Lange, Bernd M
APPLICANT: Lange, Bernd M
APPLICANT: Wildung, Mark R
APPLICANT: McCaskill, David G
TITLE OF INVENTION: Nucleic and Amino Acid Sequences Relating to a No. 61'
TITLE OF INVENTION: Transketolase, and Methods for the Expression Thereof
FILE REFERENCE: No. 6190895el transketolase from peppermint
CURRENT APPLICATION NUMBER: US/09/146,221
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 60/056,033
EARLIER FILING DATE: 1997-09-02
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414 MLFALDRAGIVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROML-TTGFQHHGPAS
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                                                                                                                   ADKMHGVVKFD-AKTGKOMKTKNKTKSYTQYFABSLVABABHDDKIVAIHAAMGGGTGLN 432
                                                                                                                                                         PLAYHGVPAFDPTKDFLPKAAPSPHPTYTEVFGRWLCDWAAQDERLLGITPAMREGSGLV 353
                                        IFQKQFPDRCFDVGIAEQHAVTFAAGMAAEGLKPFCAIYSSFLQRGYDQVVHDVDLQKLP
                                                                               EFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLD 413
                                                                                                                                                                                                    KPGASLFEELGIYYIGPV---DVEDLVYIFKKVKEMPAPGPVLIHIITEKGKGYPPABIA 373
                                                                                                                                                                                                                                                                                                                     -----SPPVGAMUNYLTKVLSSKFYSSVRBBSKKALAKMPS-VWBLARKTEBHVKGMI- 236
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SEQ ID NO 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frag
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis,
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
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TYPE: PRT
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GAAIDPTLTA-----LEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQL-----GATVVN
                                                                                                                                            RYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRA
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                                                  GLAYGDGRSHHGIYDMSFLRAMPQMIICQPRSQVVFQQLLYSSLHWSSPSAIRYPNIPAP
                                                                                                                                                                                                                        -FDPTKDFLPKAAPSPHPTYTEVPGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPN 361
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US-08-311-731A-56
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: GATES, EDMARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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   VGMMNYLTKVLSSKFYSSVREESKKALAKMPSVWELA----RKTEEHVKGMIVPGTLFE 243
                                     ADGLAKAFELAGNRNRHVVÄVVGDGALTGGMCWEALNNIAATPRPVVIVVNDNGRSYAPT 273
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
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TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                       LLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVFNT 68
                                                                        PHDPIIFDTGHQAYVHKMLTGRCQDFDSLRKKAGLSGYPSRAESEHDWVESSHASTALSY 213
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ALCMAIASQURG-EDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISPP 187
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4.1e-100;
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                                             688 HASRSEVLADIGLTDQDVARRI 709
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Gapop 10.0 , Gapext 0.5
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1-deoxy-xylulose 5
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I-deoxyxytulose-5-	פי	1-deoxyxylulose-5-	hypothetical	probable dxs prote	transketolase B	1-deoxyxyiulose-5-	probable transketo	1-deoxyxylulose-5-	transketolase [im]	1-deoxyxylulose-5-	probable transketo	hypothetical prot	1-deoxyxylulose-5-	1-deoxy-D-xylulose	,

ALIGNMENTS

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Qy 360 PNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALD 419	Db 301 VPKFDPSHHSLPXSS-NTKPTFSKIFGDFLCDMAAQDPKLMAITPAWREGSGWVRFSKEY 359	241 TLPEBLGFNYIGPVDGHDVLELIKTLKNMRELKGPQFLHVMTKKGKGYAPAEKDPIGYHG	QY 180 NDMSISPEVGAMONYLTKYLSSKTYSSYREESKKALAKMESVWELAKKIEEHVKGMIVPG 239 - - - - - - - - - - - - -	GHSSTSISAALGMAIASQLRGEDKXMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILND 	Qy 60 VALHYVFNTFVDQLVWDVGHQAYPHKILTGRXERMFTIRTLGGVSAFFARDESEYDAFGV 119 :-	OY 3 LTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELT 59	Query Match 65.2%; Score 2097.5; DB 2; Length 626; Best Local Similarity 62.5%; Pred. No. 2.8e-139; Matches 391; Conservative 109; Mismatches 117; Indels 9; Gaps 3;	A;Status: preliminary A;Molecule type: DNA A,Rolecule type: DNA C,Superfamily: hypothetical protein C2814	Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: H82266	C;Accession: H82266 R;Heidelberg, J.F.; Bisen, J.A.; Melson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. Lardson, M.B.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.	RESULT 1 H82266 1-deoxyxylulose-5-phosphate synthase VC0889 [imported] - Vibrio cholerae (strain N16961 s C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Spate: 18-Aug-2000 #sequence revision 20-Aug-2000 #text change 02-Feb-2001

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C, Genetics:
A, Gene: dxs; PA4044
C, Superfamily: hypothetical protein
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A;Residues: 1-627 <STO>
A;Cross-references: GB:AE004821; GB:AE004091; NID:g9950236; PIDN:AAG07431.1; GSPDB:GN00!
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R;Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                     VAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVG 425
                                                                                                                                                     DFLFKAAP--SPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRYFD
                                                                                                                                                                                                                                                                                                                                                                                                                                   AALGMAIASQLRGEDKXMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISPP 187
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                                                                                                                                                                                                                                                       NYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPTK 307
                                                                                                                                                                                                                                                                                                                                        VGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELGF 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPVDQLVMDVGHQAYPHXILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSIS 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.4%; Score 2069.5; DB 2; ilarity 63.4%; Pred. No. 2.6e-137; Conservative 100; Mismatches 117;
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: A10385
C;Access
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A;Molecule type: DNA
A;Residues: 1-619 <KUR>
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                         DGPTHAGAFDYSYMRCI PNMLIMAPADENECROMLTTGFOHHGPASVRYPRGKGPGAAID
                                                                                                     AIAEQHAVTLAAGQACQGAKPVVAIYSTELQRGYDQLIHDVALQNLDMLFALDRAGLVGP
                                                                                                                                                                                             KDFLFKAAPSPHFTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRYFDV
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                                                                         AIAEQHAVTFAAGLAIGGYKPVVAIYSTFLQRAYDQLIHDVAIQNLPVLFAIDRGGLVGA
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Pred. No. 1.7e-133;
5; Mismatches 139;
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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero,
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0554
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A; Residues: 1-620 < PAR>
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DGPTHAGAFDYSYMRCIPNWLIMAPADENECRQMLTTGFQHH-GPASVRYPRGKGPGAAI
                                                                     AIAEQHAVTLAAGQACQGAKFVVAIYSTELQRGYDQLIHDVALQNLDMLFALDRAGLVGF
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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Status: nucleic acid sequence not shown; translation A;Molecule type: DMA
A;Residues: 1-620 <BLAT>
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
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C;Superfamily: hypothetical protein C2814
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 DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                  DGQTHQGAFDLSYLRCIPEMVIMTPSDENECRQMLYTGYHYNDGPSAVRYPRGNAVGVEL
                                                                 DGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGPOHH-GPASVRYPRGKGPGAAI
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M.; Col

D.J.; Mayhew K.; Apodaca,

O157:H7, s

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A;Molecule type: DNA
A;Residues: 1-620 <HAY>
A;Residues: GB:BA000007; PIDN:BAB33B97.1; PID:g13359931; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90688
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C; Superfamily:
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                        TP-LEKLPIGKGIVKRRGEKLAILNFGTLMPEAAKVAESLNATLVDMRFVKPLDETLILS
                                                                                                                    DGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGPOHH-GPASVRYPRGKGPGAAI
                                                                                                                                                                                                 AIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVGP 426
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                                                                                                 DGQTHQGAFDLSYLRCIPEMVIMTPSDENECROMLYTGYHYNDGPSAVRYPRGNAVGVEL
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Accession: F8538
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F8538
A;Status: preliminary
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C;Superfamily: hypothetical protein C2814
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A;Residues: 1-620 <STO>
A;Cross-references: GB:AE005174; NID:g12513276; PIDN:AAG54770.1; GSPDB:GN00145; UWGP:Z05
A;Experimental source: strain O157:H7, substrain ED1933
C;Genetics:
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                                                                                                                        DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                                                                                                                                            DGQTHQGAPDLSYLRCIPEMVIMTPSDENECRQMLYTGYHYNDGPSAVRYPRGNAVGVEL
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A; Cross-references: GB; EE004037; GB:AE003849; NID:g9107394; PIDN:AAF85048.1; GSPDB:GN001 A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Abriones, M.R.S.; Bueno, K.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. ab-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrando, M.A.; Madeira, A.M.B. N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H.A.; Authors: Martins, E.M.F.; Matsbumma, A.Y.; Menok, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa J.T., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, A.F., fa Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A.Reference number: A53328
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A;Molecule type: DNA
A;Residues: 1-670 <SIM>
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A;Note: for a complete list of authors see reference number A59328 below
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                                                             PNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALD 419
                                                                                                                   VAPFDPQKGLIKAGAKK--QTYTDVFSEWLCDMAAVEPRILAITPAMREGSGLVRFSQEY
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59.3%; Pred. No. 5.9e-129;
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A;Authbors: Gnehm, C.L.; McDonald, L.A.; Small, X.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: B64172
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C;Species: Haemophilus influenzae
C;Date: 18 -Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Sep-1999
C;Accession: B64172
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A; Residues: 1-625 <TIGR>
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                                                                                                      FDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGL
                                                                                                                                                                      DPISGELPK--NNSKPTYSKIPGDWLCEMAEKDAKIIGITPAMREGSGMVEPSQRFPKQY
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C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: B81978
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Nature 404, 502-506, 2000
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C;Superfamily: hypot
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A;Experimental source: serogroup A, strain Z2491
C:Campetice:
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A;Residues: 1-637 <PAR>
A;Cross-references: GB:AL162753;
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A;Accession: B81978
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A;Reference number: A81775; MUID:20222556; PMID:10761919
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C;Species: Neisseria meningitidis
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                                                                                                                                                                                                                       AALGMAIASQLRGEDKXXXVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISPP 187
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                                        VHDIALQNLPVLFAVDRAĞI VĞADĞPTHAĞI YDISFIRCIPNMI VAAPSDENECRILIST
                                                                  IHDVALQNLDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTT
                                                                                                                                                                                                  VKYHAVAN-----LPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAIT
                                                                                                                                                                                                                                                                               SL---SLEENEGERYTGPVDGHNVENLVDVLEDLRGRKGPQLIHVITKKGNGYKLAENDP
                                                                                                                                                                                                                                                                                                                     MIVPGTLFEELGFNYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDP
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  GFQHHGPASVRYPRGKGPGAAIDPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGK 523
                                                                                                                     PAMREGSGLVEFEQRFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQL
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D81034
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Authors: A;Reference mumber: A81000; MUID:20175755; PMID:10710307
A;Accession: D81034
A;Accession: D81034
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D81034
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C;Superfamily: hypothetical protein C2814
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A,Molecule type: DNA
A,Residues: 1-637 <TET>
A,Crose references: GB:AE002536;
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    GFQHHGPASVRYPRGKGPGAAIDPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGK
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                                                                VHDIALQNI.PVLFAVDRAGIVGADGPTHAGIYDLSFLRCVPNMIVAAPSDENECRILLST
                                                                                                                                                                                                                                                                                                        SL---SLFENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPQLLHVITKKGNGYKLAENDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AALGMAIASQLRGEDKKWVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISPP 187
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                                                                                                IHDVALQNIDMLFALDRAGIVGFDGFTHAGAFDYSYMRCIPNMIMAPADENECRQNLTT 463
                                                                                                                                                                                                                           VKYHAVAN-----LPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAIT
                                                                                                                                                                                                                                                                                                                                                                                   VGALPKYLASNVVRDMHGLLSTVKAQTGKVLDKIPGAMEPAQKVEHKIKTLAEEAEHAKQ 244
                                                                                                                                               PAMREGSGLVEFEORFFDRYFDVGIAEQHAVTFAGGLACEGMKFVVAIYSTFLORAYDQL
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B, strain MC58
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A;Residues: 1-608 <STO>
A;Cross-references: GB:AD000398; (A)Cross-references: GB:AD000398; 
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R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa,
Nature 407, 81-86, 2000
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A;Status: preliminary
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
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                                                                                                                                                                                                                                                                               RYFDVAIAEQHAVTLAAGQACQGAXPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAGLGMSIAAEKEGRARKTICIIGDGAMTAGMAFEAINHAGEIQSNLLVILNDNQMSISR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIGLEDREVEQUERELLSLYGLDSKGI
VGELLMP-MURIPIGKSLIKRRGKKIAILNFGILLHNAYCAAEKLDATLVDMRFVKPLDK
                                                                                                                                                             GIVGNDGQTHQGVFDLAYLRCIPGIVIMTPSNENECRQMLYTGYMHNKGPSVVRYPKGYG
                                                                                                                                                                                                        GLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFOHH-GPASVRYPRGKG
                                                                                                                                                                                                                                                    OYFDVAIAEQHAVTFAAGLAISGYKPVVSIYSTFFQRAYDQLIHDIALQKLSVLFAVDRA
                                                                                                                                                                                                                                                                                                                                                  SRD--
                                                                                                                                                                                                                                                                                                                                                                        AFDPTKDFLPKAAPSPHPTYTEVFGRWL/CDMAAQDERLLGITPAMREGSGLVEFSQKFPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEELGENYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVGALNKHL-KILRSVQNTQKNRKKIRLLNKKLFFK-----DKRIQNH---SISFNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVGAMNNYLTKVLSS-----KFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTPFDNLLWDTGHQAYPHKILTGRGEKINSIRKKNGLHSFPCREESEYDSLSVGHSSTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YPILSFANSVENLRLLSVEOLFOLCFELREYLLDVVSISKGHFASGLGVVEITVALHYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLGVADTVTGHGDPKKLLDDLGLSABAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLGATVVNMRFVKPFDQALVLELARTHDVFVTVEENVLAGGAGSAINTFLQAQKVLMPVC
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                                                                                                               PGAAIDPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       PSNLGCKYLGPFDGHNIFSIINTLKKIKNKKGTYLLHLVTKKGKGYLPABLNPIKWHTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C2814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                -SVSKSLSYSDVFGTWLCEIAAFDKKLIAITPAMCEGSGMVKFSRLFPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3%; Score 1667; DB 2;
3%; Pred. No. 4.4e-109;
118; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSPDB: GN00144
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C;Superfamily: hypothetical protein C2814
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A; Title: The complete genome of the hyperthermophilic bacterium A; Reference number: A70300; MUID:98196666; PMID:9537320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A70376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Deckert,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Aquifex aeolicus;Date: 08-May-1998 #text_change 24-Sep-1999;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 24-Sep-1999;Accession: A70376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Molecule type: DNA
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                                                                                                                                         V---PTEGFKKIBIGTWEELLEGEDCVILAVGYPVYQALRAAEKLYKEGIRVGVVNARFV
                                                                                                                                                                                                                                                                                                                                                              YEDVALAEQHAVTLAAGQACQGAKDVVALYSTFLQRGYDQLLHDVALQNLDMLFALDRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                         ELGFNYIGPIDGHDIKALEDTLNNVKDIKGPVLLHVYTXKGKGYKPABENPVKWHGVAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELGFNYFGBIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAFAEKDFLAYHGVPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPPVGAMNYLTKVLSSKFYSSVREESKKALAKM-PSVWELARKTEEHVKGMIVPGTLFE
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         SREELLSLVGLDSKGI 61:
                                                                                         KPPDQALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQXVLMPVCNIGLPDRFVEQG
                                                                                                                                                                                   AAIDPT--LTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQL-----GATVVNMRFV
                                                                                                                                                                                                                                   LVGDDGPTHHGVFDLSYLRCVPNMVVCAPKDEQELRDLLYTGIYSGKPFALRYPRGAAYG
                                                                                                                                                                                                                                                                          LVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQHHGPASVRYPRGKGPG
                                                                                                                                                                                                                                                                                                                        FEDVGIAEQHACTFAAGLAAEGLRPVAAYYSTFLQRAYDQVIHDVALQNLPVTFAIDRAG
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                                                  KPMDEKMLRDLANRYDTFITVEDNTVVGGFGSGVLEFFAREGIMKRVINLGVPDRFIEHG
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Pred. No. 8.6e-106;
5; Mismatches 174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN: AAC07004.1;
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A;Status; preliminary
A;Status; preliminary
A;Residues: 1-643 <KUR>
A;Residues: 1-643 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52679.1; PID:gl7983505; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1498
A;Map position: I
C;Superfamily: hypothetical protein C2814
C;Keywords: carbon-oxygen lyase; hydro-lyase
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AD3439
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C; Date: 01-Feb-2002
C; Accession: AD3439
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C;Species: Brucella melitensis
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Best Local (
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                                                        HDLIRRLAREHEVLVMVBEGAV-GGFGSHVLQFLATDGLLDRGFKVRALTLFDIYQDHGK
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                                                                                          QALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVL---MPVCNIGLPDRFVEQGS
                                                                                                                             LPERGSVLEIGKGRIVREGIKVALLSFGTRLQECLAAAEELGAAGISTIVADARFAKPLD
                                                                                                                                                                IDPTLTALEIGKAEVRHIGSRIAILAWGSMVTPAVEAGKQLGA----TVVNMRFVKPFD
                                                                                                                                                                                                   ADGPTHAGSFDTGFLAALPGFVVMAASDEAELRHMVRTAAEYDEGPISFRYPRGDGVGVD
                                                                                                                                                                                                                                  PDGPTHAGAFDYSYMRCIPHMLIMAPADENECROMLTTGFQH-HGPASVRYPRGKGPGAA
                                                                                                                                                                                                                                                                         VGIAEQHAVTFAAGLASEGYKFFCAIYSTFLQRGYDQVVHDVSIQNLFVRFFIDRAGLVG
                                                                                                                                                                                                                                                                                                      VAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVG
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51.4%; Pred. No. 9.66
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A;Cross-references: GB:AE005673; NID:gl3423547; PIDN:AAK24039.1; GSPDB:GN00148
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C; Superfamily:
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QDQDKPDAMYAQAGLDAEGIL
                                                                             VKPFDQALVLELARTHDVFVTVBENVIAGGAGSAINTFLQAQKVL---MPVCNIGLPDRF
                                                                                                                                  GPGAAIDPTLTALBIGKAEVRHHGSRIAILAWGSMVTPAVE-----AGKQLGATVVNMRF
                                                                                                                                                                                                                  ERTFDVGIAEQHAVTFAAGMAADGMKPFAAIYSTFLQRGYDQVVHDVAIQGLPVRFAMDR
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                                                                                                                                                                                                                                                                       VKPDVVTGQQQKAAGGP-PSYTKVPAQELIKQAEKDDKIVAITAAMPSGTGLDLFGKAFP
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                          VEQUEREELLSTAGTDSKCIT
                                                    AKPLDLDLLLRLAREHRAIITVEEGSM-GGFGAFVLQALAQHGALDRGLKIRTLCLPDVF
                                                                                                       CLGLDMPALAEPLEIGKGRIVREGTSVAIVSFGTRLSESLKAADLLAARGLSATVCDARF
                                                                                                                                                               AGLVGADGPTHAGSPDIGFMGALPGMVLMAAADEVELARMVATAAEIDDRPSAFRYPRGE
                                                                                                                                                                                        AGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQ-HHGPASVRYPRGK 479
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97; Mismatches 196; Indels
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Search completed: January 29, 2004, 15:55:29 Job time : 20.2424 secs

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15 xylella fas
15 haemophilus
17 wiggleswort
13 neisseria m
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Best Local
SEQUENCE FROM N.A.

STRAIN-EI TOR N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

podson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayyam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
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QSKT13;
QSKT13;
QSKT13;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Dast annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7) (1-deoxy-D-xylulose-5-phosphate synthase) (DXP synthase) (DXPS)
                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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Vibrio cholerae.
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Pred. No. 2.9e-141;
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Pfam; PF02780; transketolase_C; 1.
Ffam; PF02780; transketolase_C; 1.
FIGRAMs; TIGR00204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
Transferase; Flavoprotein; Thiamine pyrophosphate; Isoprene biosynthesis; Thiamine biosynthesis; Comp SEQUENCE 626 AA; 68346 MW; 5E83BF99EE8C51C9 CR
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HAMAP, MF 00315; .; 1.
InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase C.
InterPro; IPR005475; Transketolase CR.
InterPro; IPR005474; Transketolase N.
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Fraser C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homodimer (By similarity).
SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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X MEDLINE-20437337; PubMed=10984043;

X MEDLINE-20437337; PubMed=10984043;

X MEDLINE-20437337; PubMed=10984043;

X Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., A. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

INATURE 406:959-964 (2000).

Nature 406:959-964 (2000).

Lord ACTIVITY: Pyruvate and glyceraldehyde 3-phosphate to yiel of the coxy-D-xylulose-5-phosphate (DXP).

C --- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1.

COPACTOR: Binds 1 thiamine pyrophosphate per subunit (By estation).
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Bacteria; Proteobacteria;
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16-OCT-2001 (Rel. 40, Last sequence update)
15-OST-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
deoxyylulose-5-phosphate synthase) (DXP synthase) (
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s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                              SUBUNIT: Homodimer (By similarity). SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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InterPro; IPR005476; Transketolase_C.
InterPro; IPR005476; Transketolase_CR.
InterPro; IPR005475; Transketolase_N.
InterPro; IPR005475; Transketolase_N.
Pfam; PP02779; transket pyr; 1.
Pfam; PF02779; transketolase_C; 1.
TIGRPAMS; TIGR00204; dxs; 1.
TIGRPAMS; TIGR00204; dxs; 1.
PROSITE; PS00802; TRANSKETOLASE_1; FALSE_NEG.
PROSITE; PS00802; TRANSKETOLASE_2; FALSE_NEG.
        QBEGR9;
                        DXS_SHEON
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PIR; G83139; G83139.
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Isoprene biosynthesis; Thiamine biosynthesis; Complete
SEQUENCE 627 AA; 68049 MW; EBEF04296FF6D57D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF282878; AAF97240.1;
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an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALGMAIASQLRGEDKKOVAIIGAGSITGGMAYEAMNHAGDVNANELVILNDNDMSISPP 187
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                          STANDARD;
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Pred. No. 3.96
                          PRT;
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                            622
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15-SEP-2003
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                                                                                                                                                                                       PROSITE; PS00801; TRANSKETOLASE 1; 1.

PROSITE; PS00802; TRANSKETOLASE 2; 1.

Transferase; Flavoprotein; Thiamine pyrophosphate;

Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome

SEQUENCE 622 AA; 68083 MW; BE681CO1BEASEFB4 CRC64;
                                                                                                                                                                                                                                                                   Pfam; PF02780; transketolase C; Pfam; PF02779; transket pyr; 1. TIGRFAMS; TIGR00204; dxs; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deoxyxylulose-5-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-deoxy-D-xylulose
                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Hor
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Catalyzes the acyloin condensation reaction bet atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).
CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphadeoxy-D-xylulose 5-phosphate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: Binds 1 thiamine pyrophosphate per
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                                                                                                                                                                                                                                                                                                                                                                                                      AE015598; AAN54586.1; -. S01525; -.
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                                                                                                                                            Similarity
VYNTPFDRLIWDVGHQAYPHKILTGRRDRMHTIRQKNGLHPFPWREESEYDTFSVGHSGT
                           VPNTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSST
                                                                                TDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHY
                                                                                                                                                                                                                                                                                                                _00315; -; 1.
IPRO05477; Dxs.
IPR005476; Transketolase_C.
IPR005475; Transketolase_CR.
IPR005474; Transketolase_N.
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homodimer (By similarity). TY: Belongs to the transketolase family. DXPS subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nonmevalonate terpenoid Biosynthetic pathway to
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                                                                                                                                           63.5%;
                                                                                                                             105;
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Pred.
                                                                                                                             Mismatches
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No. 3
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thiamine and
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                                                                                                                 DIQLDAEGMLAQINAYLA
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STRAIN-KIM5 / Biovar Mediaevalis;
MEDLINE-22137863; PubMed-12142430;
Deng W., Burland V. plumbara
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MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.

"Genome sequence of Yersinia pestis, the causative agent of pla

"Rature 413:523-527(2001)."
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V Straley S.C., McDonough K.A., Nilles M.L., Matson J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
15-FBB-2003 (Rel. 42, Last annotation update)
1-deoxy-D_xylulose 5-phosphate synthase (EC 2
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STRAIN=CO-92
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DXS OR YPO3177 OR Y1008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
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Best Local :
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HAWAP; MF 00315; -; Dxs.

InterPro; IPR005476; Transketolase C.

InterPro; IPR005475; Transketolase CR.

InterPro; IPR005475; Transketolase CR.

InterPro; IPR005475; Transketolase CR.

InterPro; IPR005474; Transketolase CR.

Pfam; PF02790; transket pyr; 1.

Pfam; PF02780; transketolase C; 1.

TIGRFAMS; TIGR00204 dxs; 1.

TIGRFAMS; TIGR00204 dxs; 1.
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"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).

1. EUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).

1. CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2).

1. COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By similarity).

1. Similarity Victorians Personnel Historynthesis pathway; first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00801; TRANSKETOLASE 1; 1.

PROSITE; PS00802; TRANSKETOLASE 2; 1.

Transferase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Comp
SEQUENCE 619 AA; 67673 MW; B528BE47650AA296 CR
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                                                                                                                                                                                                                                   FNYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPT
                                                                                                                                                                                                                                                                                                   PVGAMMNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTPVDQLVWDVGHQAYPHKILTGRXERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVF
AIAEQHAVTLAAGQACQGAKPVVAIYSTFIQRGYDQLIHDVALQNLDMLFALDRAGLVGP 426
                                                                                                 SGTLPK-SQSSLPTYSKIFGEWLCETAAKDSKLMAVTPAMREGSGMVRFSREYPQQYFDV
                                                                                                                                                                                                 FNY I GPVDGHDVHTLTQTLKNMRDLKS PQLLHIMTKKGKGYAPABKDPIGWHAVPKFDPA
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pyridoxol; first
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STRAIN-Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMedt G. III, Mayhew G.F., Rose D.J.,
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21534947; PubMed=11677608;
Parkhill J., Dougan G., James R.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of a enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deoxyxylulose-5-phosphate synthase)
DXS OR STY0461 OR T2441.
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15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy_D-xylulose 5-phosphate synthase (EC 2.2.1.7)
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15-SEP-2003
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Bnterobacteriaceae; Salmonella.
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                                                                                     step.
SUBJUNT: Homodimer (By similarity).
SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
                                                                                                                                             PATHWAY: Biosynthetic
                                                                                                                                                           similarity).
PATHWAY: Non
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                                                                                                                                          Nonmevalonate terpenoid Biosynthetic pathway to
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                                                             It is produced through a collaboration
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thiamine and
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                                                                                                                                             pathway; first step.
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SOURCE SERVICE RESULȚ 7
DXS_SALTY
ID DXS_SALTY
AC Q8ZRD1;
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Matches 375
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Piam; PR02780; transketolase C; 1.
TIGRPAMs; TIGR00204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE 1; 1.
PROSITE; PS00802; TRANSKETOLASE 2; 1.
Transferase; Plavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome.
INIT_MET 0 0 BY SIMILARITY.
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HAMAP; MF 00315; -; 1.

InterPro; IPR005477; Dxs.

InterPro; IPR005476; Transketolase C.

InterPro; IPR005475; Transketolase CR.

InterPro; IPR005474; Transketolase N.
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            SAALGWAIASQLRGEDKKWYAIIGDGSITGGWAYEAMNHAGDVNANLLVILNDNDWSISP
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.deoxyxylulose-5-phosphate synthase) (DXP synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:852-856(2001).

Nature 413:852-856(2001).

Propertion: Catalyzes the acyloin condensation reaction between atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yi 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).

Propertic ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = deoxy-D-xylulose 5-phosphate + CO(2).

Representation of the pyrophosphate per subunit (By -1-COPACTOR: Binds 1 thiamine pyrophosphate pyrophosphate pyrophosphate pyrophosphate pyrophosphate pyrophosphate pyrophosphate pyrophosphate pyrophosphate p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
MCClelland M., Sonderson K.E., Spieth J., Clifton S.W., Layman D.,
Courttley L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deoxyxylulose-5-phosphate DXS OR STM0422.
                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00801; TRANSKETOLASE 1; 1.

PROSITE; PS00802; TRANSKETOLASE 2; 1

Transferase; Plavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome,
INIT MET

0

BY SIMILARITY.

SEQUENCE 619 AA; 67336 MW; FB3525B91DB6F346 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eb the European Bioinformatics Institute. There are no restricted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF 00315; -; 1.
InterPro; TPR005477; Dxs.
InterPro; TPR005476; Transketolase_C.
InterPro; TPR005475; Transketolase_CR.
InterPro; TPR005474; Transketolase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02779; transket pyr; 1.
Pfam; PF02780; transketolase_C; 1.
TIGRFAMs; TIGR00204; dxs; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Homodimer (By similarity).
SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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NTPFDQLIWDVGHQAYPHKILTGRRDKIGTIRQXGGLHPFPWRGESEYDVLSVGHSSTSI
                                  NTPVDQLVMDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI
                                                                                                                        YPTIALVDSTQBLRLLPKESLPKLCDELRRYLLDSVSRSSGHFASGLGTVELTVALHYVY
                                                                                                                                                        YPLLKNIHTPADIRALSKDQLQQLADBYRGYLTHTVSISGGHFAAGLGTVELTVALHYVF
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                          Score 2013.5; DB 1;
Pred. No. 3.4e-134;
6; Mismatches 131;
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                                                                                                                         RC STRAIN-GMILOO;

RX MEDLINE-21681879; PubMed=11823852;

RA Salanoubat M., Genin S., Artiguenave P., Gouzy J., Mangenot S.,

RA Arlat M., Billault A., Brottiter P., Camus J.C., Cattolico L.,

RA Arlat M., Billault A., Brottiter P., Camus J.C., Cattolico L.,

RA Arlat M., Billault A., Brottiter P., Camus J.C., Cattolico L.,

RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

RA Gaspin C., Lavie M., Moisan A., Robert C.,

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RA Gaspin C., Lavie M., Moisan A., Robert C.,

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RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

RA Gaspin C., Lavie M., Moisan M., Mo
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08XX95;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-Dxylulose 5-phosphate synthase (BC 2.2.1.7)
deoxyxy-ulose-5-phosphate synthase) (DXP synthase)
DXS_OR_RSC2221 OR_RS01378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                      COFACTOR: Binds
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HAMAP; MF_00315; -; 1.

InterPro; IPR001017; Dehydrogenase_E1.

InterPro; IPR005476; Dxs.

InterPro; IPR005476; Transketolase_C.

InterPro; IPR005475; Transketolase_CR.

InterPro; IPR005475; Transketolase_CR.

InterPro; IPR005474; Transketolase_CR.

InterPro; IPR005474; Transketolase_CR.

Ifam; PP00779; transketolase_C; 1.

Pfam; PP02780; transketolase_C; 1.

Pfam; PP02780; transketolase_C; 1.

IIGRPAMS; TIGR00204; dxs; 1.

PROSITE; PS00801; TRANSKETOLASE_I; 1.

PROSITE; PS00802; TRANSKETOLASE_I; 1.
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; Pred. No. 7.9e-134;
92; Mismatches 134;
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01-NCV-1997 (Rel. 35, Created)
01-NCV-1997 (Rel. 35, Last sequence update)
01-NCV-1997 (Rel. 35, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D-1-deoxyxylulose 5-phosphate, a common precursor thiamin, and pyridoxol biosynthesis."; proc. Natl. Acad. Sci. U.S.A. 95:2105-2110(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deoxyxylulose-5-phosphate synthase) pxs OR B0420.
                                                                                    J. Bacteriol. 182:891-897(2000).

-!- FUNCTION: Catalyzes the acyloin condensation reastoms 2 and 3 of pyruvate and glyceraldehyde 3-p.

1-deoxy-D-xylulose-5-phosphate (DXP).

-!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde deoxy-D-xylulose 5-phosphate + CO(2).
                                                                                                                                                                                                                                                                                                            MEDLINE=98058734; PubMed=9371765; Sprenger G.A., Schorken U., Wiegert T., Grolle S., de Sprenger G.A., Schorken U., Wieger-Meyer S., Sahm H.; Taylor S.V., Begley T.P., Bringer-Meyer S. Sahm H.; "Identification of a thiamin-dependent synthase in Es required for the formation of the 1-deoxy-D-xy/lulose precursor to isogrenoids, thiamin, and pyridoxol."; Proc. Natl. Acad. Sci. U.S.A. 94:12857-12862(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                  Kuzuyama T., Takagi M., Takahashi S., Seto H.;
"Cloning and characterization of 1-deoxy-D-xylulose 5-phosphate
synthase from Streptomyces sp. strain CL190, which uses both the
mevalonate and nonmevalonate pathways for isopentenyl diphosphat
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-6, AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of a gene from
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                                                                                                                                                                                    biosynthesis.";
                                                                                                                                                                                                                                                                 MEDLINE=20115529; PubMed=10648511;
                                                                                                                                                                                                                                                                                CHARACTERIZATION
                               PATHWAY:
                                                                          COFACTOR: Binds 1 thiamine
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                             Nonmevalonate terpenoid Biosynthetic pathway to
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000148; AA0
EMBL; U82664; AAB40
PIR; D64771; D6477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- MISCELLANEOUS: Optimal temperature is 42-44 degrees Ceisius and optimal pH is 7.5-8.0.
-:- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005474; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
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Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00801; TRANSKETOLASE 1; 1.
PROSITE; PS00802; TRANSKETOLASE 2; 1.
Transferase; Plavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Manganese; Magnesium;
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PF02780; transketolase_C; 1.
AMs; TIGR00204; dxs; 1.
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                           DPTLTALBIGKAEVRHHGSRIAILANGSNVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                                                           DGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQHH-GPASVRYPRGKGPGAAI
                                                                                                               AIAEOHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVGP
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AAC73523.1; -.
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114; Mismatches
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Pred. No. 2.86
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X MEDLINE-22388234; PubMed=1247157;
X MEDLINE-22388234; PubMed=1247157;
X MEDLINE-22388234; PubMed=1247157;
X Melch R.A., Burland V., Plunkett G. III. Redford P., Roesch P.,
X Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
X Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
X Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
X Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
X Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
X "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
X Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
X Proc. Natl. Acad. Sci. U.S.A. 99:1702
Query Match
Best Local
                                                                                       EMBL; AE016756; AAN79009.1; -.

HAMAP; MF 00315; -; 1.

InterPro; IPR005477; Dxs.

InterPro; IPR005476; Transketolase_C.

InterPro; IPR005476; Transketolase_CR.

InterPro; IPR005474; Transketolase_N.

Pfam; PF02780; transketolase_N.

Pfam; PF02780; transketolase_S.

IGROPTTP; transketolase_I.

PF03178; PF00801; TRANSKETOLASE_I; 1.

PROSITE; PF00801; TRANSKETOLASE_I; 1.

PROSITE; PF00802; TRANSKETOLASE_I; 1.

INTERPROSITE; PS00802; TRANSKETOLASE_I; 1.

PROSITE; PF008002; TRANSKETOLASE_I; 1.

INTERPROSITE; PS00802; TRANSKETOLASE_I; 1.

INTERPROSITE; PS00802; TRANSKETOLASE_I; 1.

PROSITE; PF008002; TRANSKETOLASE_I; 1.

INTERPROSITE; PS00802; TRANSKETOLASE_I; 1.

INTERPROSITE; PS00802; TRANSKETOLASE_I; 1.

INTERPROSITE; PS00801; TRANSKETOLASE_I; 1.

INTERPROSITE; 
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Q8FKB9;
15-SEP-2003
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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SIMILARITY: Belongs to the transketolase family.
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STRAIN-0157:H7 / ED1933 / ATCC 700927;
STRAIN-0157:H7 / ED1933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
Medline-21074935; PubMed-11206551;
Merna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
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Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXS OR Z0523 OR ECS0474.
                                                                                                                                                                                                                                        NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                          Escherichia coli 0157:H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TP-LEKLPIGKGIVKRRGEKLAILNPGTLMPEAAKVAESLNATLVDMRFVKPLDEALILB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPTLTALBIGKAEVRHKOSRIAILAMGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGPTHAGAFDYSYMRCIPNWLIMAPADENECRQWLTTGPQHH-GPASVRYPRGKGPGAAI
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                                                                                                                                                                                                                                                                                             Enterobacteriales;
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X Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

A Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T.,

A Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

A Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

"Complete genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

DNA Res. 8:11-22(2001).

C -1- FUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).

C -1- COTACTOR: Binds 1 thiamine pyrophosphate per subunit (By
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00315; -; 1.
InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005475; Transketolase_CR.
InterPro; IPR005474; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
Pfan; PF02779; transket_pyr; 1.
Pfan; PF02780; transketolase_C; 1.
TICRFAMS; TICR00204; dxs; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
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STRAIN=0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00801; TRANSKETOLASE 1; 1.
PROSITE; PS00802; TRANSKETOLASE 2; 1.
Transferase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Comp
INDIT_MET 0

BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B90688; B90688.
F85538; F85538.
                                                                                                                               127
                                                                                                                                                                                                                                                                                                                                                 368;
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
NVGALNNHLAQLLSGKLYSSLREGGKKVFSGVPPIKELLKRTEEHIKGMVVPGTLFEELG
                                                                           PVGAMMNYLTKVLSSKEYSSVREBSKKALAKMPSVWELARKTEEHVKGMIVPGTLEEELG
                                                                                                                               SAGIGIAVAAEKEGKURRTVCVIGDGAITAGMAPEAMNHAGDIRPDMLVVLNDNEMSISE
                                                                                                                                                        SAALGMAIASQLRGEDKKKVAIIGDGSITGGMAYEAMNHAGDVNANLLYILNDNDMSISP
                                                                                                                                                                                                                                 NTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI
                                                                                                                                                                                                                                                                                                   YPLLKNIHTPADIRALSKDQLQQLADBYRGYLTHTVSISGGHFAAGLGTVELTVALHYVF
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                                                                                                                                                                                                                                                                          YPTLALVDSTQELRLLPKESLPKLCDBLRRYLLDSVSRSSGHFASGLGTVELTVALHYVY
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                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homodimer (By similarity).
TY: Belongs to the transketolase family. DXPS subfamily
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59.8%;
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                                                                                                                                                                                                                                                                                                                                                 Score 1995.5; DB 1
Pred. No. 6.3e-133;
5; Mismatches 129;
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Binds

pyrophosphate

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similarity)

Nonmevalonate terpenoid biosynthesis Biosynthetic pathway to thiamine and

pathway; first pyridoxol; firs

step

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                                                                                                                                                                                                                                                                                                                                            RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RC MEDDINE=22022145; PubMed=12024217;

RX MEDDINE=22022145; PubMed=12024217;

RX MEDDINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Canargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Bi-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., Ell-Dorry H.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Mayaki C.Y., Moon D.H.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Percira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Prindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RT Tindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RT Thost specificities ",

RT host specificities ",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ULT 12
XANCP
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28-FEB-2003
15-SEP-2003
                                                                                                                                                   host specificities.",
Nature 417.459-463 (2002).
Nature 417.459-463 (2002).

-i- FUNCTION: Catalyzes the acyloin condensation reaction between atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yi -deoxy-D-xylulose-5-phosphate (By similarity).

-i- CATALYTIC ACTUVITY: Pyruvate + D-glyceraldehyde 3-phosphate = CATALYTIC ACTUVITY: CATALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deoxyxylulose-5-phosphate synthase)
DXS OR XCC2434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8P815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kanthomonas campestris (pv. campestris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XANCP
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Best Local Sim
Matches 378;
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R HAMAP; MF 00315; -; 1.

R InterPro; IPR005477; Dxs.

InterPro; IPR005475; Transketolase_C.

InterPro; IPR005475; Transketolase_CR.

InterPro; IPR005474; Transketolase_N.

Pfam; PF02779; transket_pyr; 1.

R Pfam; PF02780;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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                                                                                                                                                                                                                                                                                                                                               RAGIVGPDGPTHAGAFDYSYMRCIPNMLIMAFADENECROMLTTGFQHHGPASVRYPRGK 479
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                                                                                                                                                 QALVIELARTHDVFVTVEENVIAGGAGSAINTFLQAQXVLMPVCNIGLPDRFVEQGSREB
                                                                                                                                                                                                                                                                                                                RGGVVGPDGATHAGNLDLSPLRCVPHAVVMAPADEAECROMLTTGLRYEGPAAVRYPRGT
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LLAEAGIDQAGIRAAV
                                                  LLSEVGLDSKGILATI 615
                                                                                                    KAMLLELAKCHBAFVSIEDNVVÄGGÄGSGVSELLNÄBGVLMPMLHLGLPDSFQHHASRED
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Pred. No. 1.7e-132;
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RX MEDLINE-2002/45; Pubmedel 2014217;
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., Containho L.L., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Christo-Santos J.R., El-Dorry H.,
RA Cimarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Christo R.C.C., Ferro M.I.T.,
RA Faria J.B., Perreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Faria J.B., Merreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri B.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Xishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Machado M.A., Madeira R.M., Martinez-Rossi N.M.,
RA Martins E.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Takkta M.A., Tamura R.B., Teixeira M.C., Oliveira V.R.,
RA Martins E.C., Kitajima J.P.;
RA Spinola L.A.F., Takkta M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Spinola L.A.F., Takkta M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Spinola L.A.F., Takta M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Stubal J.C., Kitajima J.P.;
RA Stubal J.C
R HAMAP; MS 00315; -; 1.

R HAMAP; MS 00315; -; 1.

R InterPro; IPR005477; Dxs.

R InterPro; IPR005476; Transketolase_C.

R InterPro; IPR005475; Transketolase_CR.

R InterPro; IPR005474; Transketolase_CR.

R InterPro; IPR005474; Transketolase_C.

R Pfam; PF02779; transket pyr; 1.

R Pfam; PF02780; transket pyr; 1.

R Pfam; PF02780; transketolase_C; 1.

R Pfam; PF02780; transketolase_C; 1.

R Pfam; PF02780; transketolase_C; 1.

R Pf0SITE; PS00801; TRANSKETOLASE 1; 1.

R PROSITE; PS00802; TRANSKETOLASE 1; FALSE NEG.

R PROSITE; PS00802; TRANSKETOLASE 1; Complete propopolate; Complete propopolate; Talse propopolate; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8PJG7;
28-FEB-2003
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DXS OR XAC2565.
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STRAIN=306 / ATCC 13902 / XV 101;
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thiamine and
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RESULT
DESCRIPTION
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PASMU
  MEDLINE-21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S.,
"Complete genomic sequence of Pasteurella multocida Pm70."
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-i- FUNCTION: Catalyzes the acyloin condensation reaction atoms 2 and 3 of pyruvate and glyceraldehyde 3-phospha
                                                                                                                                                                                                                                                                  DXS_PASMU STANDARD; PRT; 614 AA.

P57848;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
deoxyxylulose-5-phosphate synthase) (DXP synthase)
DXS OR PM0532
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                           Pasteurella multocida.
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61.4%; Pred. No. 2.8e-132;
tive 91; Mismatches 142;
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Matches 369
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CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate
deoxy-D-xylulose 5-phosphate + CO(2).
COPACTOR: Binds 1 thiamine pyrophosphate per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homodimer (By similarity). SIMILARITY: Belongs to the transketolase
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                                                                                                                                                                                                                                                                HLSGOLPKS--NTTPTYSKIFGDWLCEWAENDEXLIGITPAMRECSGMVEFSNRFPQQYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYPLIKNIHTPADIRALSKOQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYV
           DVALAEQHAVTFAAGLAIGGYKPVVAIYSTFLQRAYDQVIHDVAIQNLPVLFAIDRAGVV
                                                                                                                                                                                                                                                                                                                                               LGENYIGPIDGHDVEMLVSTLENLXDLTGPVPLHVVTKKGKGYAPAEKDPLAYHGVPAFD
                                                                                                                                                                                                                                                                                                                                                                                                                                        ENVGALNNHLARLLTGSFYSSIREGGKKILSGMPPIKEFVKKTEEHVKGFVSPVGTMFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPVGAMNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVP-GTLFEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTS
                                                 IDPTLTALBIGKAEVRHIGSRIAILAWGSMVTPAVEAGKQLGATVVNWRFVKPFDQALVL
                                                                                            GADGQTHQGAFDISFLRCIPNMVIMTPSDENECRQMLYTGYKLNQPAAVRYPRGNAIGVE
                                                                                                                   GPDGPTHAGAEDYSYMRCIPNMLIMAPADENECROMLTTGFQHHGPASVRYPRGKGPGAA
                                                                                                                                                                                                         DVAIAEQHAVTLAAGQACQGAKPVVAIYSTFIQRGYDQLIHDVALQNIDMLFALDRAGLV
                                                                                                                                                                                                                                                                                    PTKDFLFKAAPSPHFTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFFNRYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.2%; Score 1969; DB 1; 60.1%; Pred. No. 4.5e-131; tive 108; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biosynthesis
thiamine and
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D3 CRC64;
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HLDEAGIETQIKNF GLDSKGILATIEQF 618

613

QIAQTHDLIVTLEENVIQEGAGSAVAEVLHSQQHQTKLLQLGLPDFFIPQGTQQEILADL

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Bacteria; Proteobacteria;
Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                    Xylella fastidiosa.
S SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL outstati European Bioinformatics Institute. There are no restrictions on European Holinformatics Institute as a long as its content is in no
                                                                                   FUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyravate and glyceraldehyde 3-phosphate to yiel 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).

CATALYTIC ACTIVITY: Pyravate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2).

COPACTOR: Binds 1 thiamine pyrophosphate per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                               XYLFA
                                       SUBUNIT: Homodimer (By similarity). SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
                                                              PATHWAY: Nonmevalonate PATHWAY: Biosynthetic
                                                             Nonmevalonate terpenoid Biosynthetic pathway to
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            Gammaproteobacteria; Kanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                               biosynthesis
thiamine and
                                                              pathway; first
pyridoxol; first
                          a collaboration
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Best Local :
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InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase C.
InterPro; IPR005475; Transketolase CR.
InterPro; IPR005475; Transketolase CR.
InterPro; IPR005474; Transketolase N.
Pfam; PF02779; transketolase C; 1.
Pfam; PF02780; transketolase C; 1.
TIGRPAMS; TIGR00204; dxs; 1.
TIGRPAMS; TIGR00204; dxs; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00801; TRANSKETOLASE 1; 1.
PROSITE; PS00802; TRANSKETOLASE 2; FLISE NEG.
Transferase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete
SEQUENCE 635 AA; 68408 MW; 18567FA8CDDDDBZE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                      VPAFDPTKDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVFNTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STCYPRLSRIQIPEDLRTFQESELRAVADELRNYLIESVGLSGGHFAAGLGVVELTIALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIDYPLIKNIHTPADIRALSKODLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALH
                                                                                                                                                                                                                                                                                                                                                                                                       MSISEAVGGLTKWLGRATGSKALNAIREGGKRIFGDKKTNATARFLRRWEEHWKGMFVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                   MSISPPVGAMNNYLTKVLSSKFYSSVREESKKALA--KMPSVWELARKTEEHVKGMIVPG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSISAALGMAIVAQRHGDERKVVAIIGDGAMTAGMAYEALNHAGGMSPAPNLLVILNDNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSISAALGMAIASQLRGEDKKKVALIGDGSITGGMAYEAMNHAGDVN--ANLLVILNDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLYCTPIDHLVWDVGHQTYPHKILTGRRDKISTVKHQGGLAPFPKREESIYDTFGVGHSS
                                                                                                              GPGVVPSAELDVLPVGVAQLKHSGTRIALLGFGVCVAPABQVGRRLGLTVVNMRPIKPLD
                                                                                                                                  GPGAAIDPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKOLGATVVNMRFVKPFD
                                                                                                                                                                                                RAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQHHGPASVRYPRGK 479
                                                                                                                                                                                                                                              PNRYFDVALAEQHAVTLAAGQACQGAKPVVAIXSTFLQRGYDQLIHDVALQNLDMLFALD 419
                                                                                                                                                                                                                                                                                                                                               TLFEELGFNYFGPIDGHDVEMLVSTLENLKOLTGPVFLHVVTKKGKGYAPAEKDPLAYHG 299
||: |:|: |: | :
|LAEAGIDAAGVYAAL
                                                       RTLLLBLARTHEGFVTIBDNVVAGGAGSGVABLLNAEGIVLPIVHLGLPDAFQQHASRED
                                                                        RGGVVGPDGATHAGNLDLSFLRCVPNMMLMAPADEABCRKMLSTGFHYSGPVAVRYPRGT
                                                                                                                                                                                                                                PQRYFDVAIAEQHAITLAAGMATQGAKPVVAIYSTFLQRGYDQLVHDVALQKLDVLFAVD
                             LLSLVGLDSKGILATI 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98;
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8e-130
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                                                                                       599
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Search completed: January 29, Job time: 12.6752 secs 2004, 15:50:38

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           830525 seqs, 258052604 residues
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3216
1 MKLTTDYPLLKNIHTPADIR.....LSLVGLDSKGILATIEQFCA 620
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Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_organ:1e:*
sp_phage:*
sp_plant:*
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sp_virus:*
sp_virus:*
sp_virus:*
sp_unclassified:*
sp_rvirus:*
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sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	43	42	41	40	39	3 8 8	37	36	35	34	y S	32	31	30	29	28	27	26					21	20	9	18	17	
522	615	689	803.5	19.	819.5	N	48	852.5	854	870	882.5	886	892.5	1030	1053	1062.5	1078.5	1097	111	1131.5	1235.5	1278.5	1311.5	1397.5	1402	402.		1418.5	
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Q9WXF0	Q9FEV6	Q8G585	QBEWX7	OMCIBO	096694	Q94CE7	Q944G7	050408	069774	Q8R606	Q9CFJ5	Q9CF08	Q97TJ5	Q8R639	Q9LFL9	Q9SNQ1	Q8CJP7	Q8VUR8	Q9F1V2	QBFPI2	Q8F153	Q8L9S4	Q9LVF5	078328	081954	Q9XH50	Q9FV39	064904	
Q9wxt0 deinococcus	Q9fev6 nicotiana t	Q8g585 bilidobacte	mycoplasm	Q8idw0 plasmodium	096694 plasmodium	Q94ce7 arabidopsis	arabidops	ycobacte	069774 roseobacter	Q8r606 fusobacteri	Q9cfj5 Lactococcus	Q9cf08 lactococcus	Q97tj5 clostridium	QBr639 fusobacteri	Q9lfl9 arabidopsis	Q9sngl oryza sativ	Q8cjp7 streptomyce	Q8vur8 kitasatospo		Q8fpi2 corynebacte	leptospir	Q819s4 arabidopsis	arabidopsi	078328 capsicum an	B1954	xh50 _	6EA36	4904 mentha F	

ALIGNMENTS

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121 GHSSTSISAALGMAICAEKEGQNRKVVSVIGDGAITAGMAFEAMNHAGDVHSDMLVILND 180	LRGEDKKMVAIIGDGSITGGM	61 VALHYVYNTPEDQLIMDVGHQAYPHKILTGRREQMPTIRQKGGLHPFPMREBSEYDTLSV 120	60 VALHYVENTEVDQLVWDWGHQAYEHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGV 119	1 MTLDISKYPTLALAETPDELRLLPKBTLPTLCDELRTYLLNSVSQSSGHLASGIGTVELT 60	ALSKOQLQQLADI	Query Match 65.7%; Score 2114; DB 16; Length 621; Best Local Similarity 63.1%; Pred. No. 1.4e-145; Matches 392; Conservative 102; Mismatches 123; Indels 4; Gaps 2;		Complete proteome.	Submitted (DEC-2002) to the EMBL/GenBank/BUBJ databases. RMBL: AE016798: AAO08845.1: -	genome sequence of	Choy H.E.;	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	10 PG :	SEQUENCE FROM N.A.	NCBI_TaxID=672;		Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	Vibrio vulnificus.	VV10315.		01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	01-MAR-2003 (TrEMBLrel. 23, Created)	ORDERS FREUTRIMONI, FAI, OLI FEI.	1

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                                                                                       Query Match
Best Local Sin
Matches 383;
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01-MAR-2003
01-MAR-2003
01-MAR-2003
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Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C.
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C.
Read T.D., Bisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Welf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Waeller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis.";
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Deoxyxylulose-5-phosphate synthase.
DXS OR S01525.
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Alteromonadaceae; Shewanella.
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                                                                                                                      Similarity
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                                                                                              Conservative
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Pred. No. 2.5e-140;
5; Mismatches 126;
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               Query Match
Best Local
                                                                           STRAIN-O6:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12473157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., &
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome
of uropathogenic Escherichia coli.;
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 4.1.3.37).
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01-MAR-2003
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                                            EMBL; ABO
Complete
SEQUENCE
                                                                                                                                                                            Akman L.,
Aksoy S.;
                                                                                                 "Genome sequence of the endocellular flies, Wigglesworthia glossinidia.", Nat. Genet. 32:402-407(2002).
                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22297718; Po
Akman L., Yamashita
                                                                                                                                                                                                                                                                                                       Wigglesworthia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
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MEDLINB=22247741; PubMed=12271122;

Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg (Paulsen I.T., Seshadri R., Nelson K.E., Kolonay J.F., Madupu R.

Paugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.

Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aker

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aker

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M

"The Brucella suis genome reveals fundamental similarities betw
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EMBL; AE014353; AAN29379.1; -.
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SEQUENCE 643 AA; 69179 MW; E42DFB422D129FEA CR
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Q8KF19;

Q1-QT-2002 (TrEMBLrel. 22;

Q1-QT-2002 (TrEMBLrel. 22;

Q1-QT-2003 (TrEMBLrel. 23;

Q1-MAR-2003 (TrEMBLrel. 23;
 SEQUENCE FROM N.A.
STRAIN=TLS / ATCC 49652 / DSM 12025;
MEDINNE=22103685; PubMed=12093901;
Eisen J.A., Nelson K.E., Paulsen I.T
                                                                          Chlorobium tepidum.
                                                                                     1-deoxyxylulose-5-phosphate DXS OR CT0337.
                                              NCBI_TaxID=1097;
                                                           Chlorobium.
                                                                   Bacteria;
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TGAMSAYLARLVSGRTYRSVREAAKQVAQKLPKFLQDKARKSEEVARAFFTGGTLFEELG
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                                                                   Chlorobia;
    Paulsen I.T.,
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Last sequence update)
Last annotation update)
synthase.
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Pred. No. 1.7e
)7; Mismatches
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                                                                    Chlorobiales;
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   Heidelberg
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es 181; Indels
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                                                                    Chlorobiaceae
    J.F.,
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InterPro; IPR005476; Transketolase C.
InterPro; IPR005475; Transketolase CR.
InterPro; IPR005474; Transketolase N.
Pfan; PP02780; transketolase C; 1.
Pfam; PF02779; transketolase C; 1.
TICREAMs; TICR00204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE 1; 1.
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EMEB: AE012812; AAM71583.1; -.
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HGSMDELYREVGLDARSLSGKILEF
                                     QGSREELLSLVGLDSKGILATIEQF 618
                                                                                                       FVKPFDQALVLELARTHDVFVTVBENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVB
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49.3%; Pred. No. 1.3e
tive 93; Mismatches
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082676; 082676; 01-NOV-1996 (TrEMBLrel. 08, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-deoxyxylulose 5-phosphate synthase.
1-deoxyxylulose 5-phosphate synthase. (Madagascar p
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Gentianales; Apocynaceae; Rauvolficideae; Vinceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005476; Transketolase_C.
InterPro; IPR005475; Transketolase_CR.
Pfam; PF02780; transketolase_C; 1.
Pfam; PF02779; transket_Dyr; 1.
TIGRENMS; TIGR00204; dxs; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
SEQUENCE 716 AA; 76793 MW; E5D75EI
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alkaloid-producing cells.",
Plant Physiol. Biochem. 38:559-566 (2000)
EMBL; AJ011840; CAA09804.2; -.
InterPro; IPR005477; Dxs.
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NVSPTVADAKFCKPLDGDLIKTLAKEHEILITVEBGSI-GGFGSHVTHFLSLTGILDGFI
                                                                           ASVRYPRGKGPGAAIDPTL--TALEIGKAEVRHKGSRIAILAWGSMVTPAVEAGKQL---
                                                                                                                   LPVRFAMDRAGI.VGADGPTHCGAFDVAYMACI.PNMIVMAPSDBAELMHMVATAAKIDDRP
                                                                                                                                 LDMLFALDRAGLVGPDGPTHAGAPDYSYMRCIPNWLIMAPADENECROMLTTGFQ-HHGP
                                                                                                                                                                            LVEFSOKFPNRYFDVALAEGHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
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                          --GATYVNMRFVKPFDQALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVL---M
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Q8DL74;
01-MAR-2003
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Makamira Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamot Makamira Y., Kaneko T., Sato S., Ikeuchi M., Kimura T., Kishida Y., Watsnabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Watsuno A., Nakazaki N., Shimpo S., Sugimoto M., Matsumoto M., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-I.";
DNA Res. 9:123-130(2002).
EMBL; AP005371; BAC08174:1; -.
Complete proteome.
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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655 AA;
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                                                                                                                             GLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFOH-HGPASVRYPRGKG
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YGVALMBEGWEPLEIGKGELLRSGEDLLLVÄYGSMVYPAMQVAEILKEHGMSÄAVINARF
                                                                                                                                                                                                                                                                                                    PDLVTGKAKPSSKPKP-PSYSKVPGETLTKLAENDPRIVGITAAMATGTGLDILQKRVPK
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                                             PGAAI-DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQL----
                                                                                                GIVGADGPTHQGMYDIAYLRCLPNMVLMAPKDEAELQRMIVTGINYTDGPIALRYPRGNG
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SEQUENCE
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Submitted (FBS-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ430048; CAD22531.1;
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Pfam; PF02779; transket pyr;
TIGRFAMs; TIGR00204; dxs; 1.
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Walter M.H., Hans J.,
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1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
-deoxy-D-xylulose 5-phosphate synthase 2 precursor.
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                                                         PLAYHGVPAFDPTKDFLPKAAPSPHPTYTEVFGRWLCDMAAQDBRLLGITPAMREGSGLV 353
                                                                                                                                                                    -VPGTLFEELGFNYFGFIDGHDVEMLVSTLENLKDL--TGPVFLHVVTKKGKGYAPAEKD
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TRANSKETOLASE_2; 1.
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Pred. No. 1.3e-96;
2; Mismatches 192; I:
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EMBL; AJ42932: CAD22155.2; -.

EMBL; HP005477; Dxs.

InterPro; IPR005476; Transketolase_C.

InterPro; IPR005475; Transketolase_C.

InterPro; IPR005475; Transketolase_C.

Pfam; PP027780; transketolase_C; 1.

Pfam; PP02779; transket_pyr; 1.

TIGRPAMs; TIGR00204; dxs; 1.

PROSITE; P900802; TRANSKETOLASE 2; 1.

PROSITE; P900802; TRANSKETOLASE 2; 1.

ROSITE; P900802; TRANSKETOLASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eupatorieae; Stevia.
NCBI_TaxID=55670;
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                                                                                                                                                                                                                                                                                                                                                                                    PLLDTINYFVHMKNLTTQDLEQLAABLRQDIVYSVANTGGHLSSSLGVVELSVALHHVFN
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                                          ATLDGPATPVGALSGALSKLQASTKFRKLREAAKSITKQIGPQAHEVAAKVDBYARGMIS
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                                                                                                    PVGAMNNYLTKVLSSKFYSSVREESKKALAKM-PSVWELARKTEEHVKGMIV
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47.7%; Pred. No. 2.5e-96;
tive 108; Mismatches 193; I
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Last annotation update)
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InterPro: IPR005476; Transketolase C.
InterPro: IPR005476; Transketolase_CR.
InterPro: IPR005474; Transketolase_N.
Pfam; PF02780; transketolase_C; 1.
Pfam; PF02779; transketolase_C; 1.
TIGRFAMS; TIGR0204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE 1; 1.
SEQUENCE 630 AA; 65840 MW; 726789DAF4
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Hamada T.,
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01-MAR-2003 (TrEMBLrel. 23,
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EMBL; AE008921; AAM48660.1; -.
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Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
"Unsuspected diversity among marine aerobic anoxygenic photo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=153809;
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; 65840 MW; 26789DAF48111C97 CRC64;
                                                                                                                                                                                                                                                                                44.7%; Score 1437.5; DB 2;
47.6%; Pred. No. 3.4e-96;
cive 100; Mismatches 195;
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                                                                                    Query Match
Best Local Sim
Matches 302;
                                                                                                                                                                                           InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005476; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
Pfam; PF02779; transketolase_C; 1.
Pfam; PF02779; transket Dyr; 1.
Pfam; PF02779; transket Dyr; 1.
PIGRPAMS; TIGR00204; dxs; 1.
PROSITE; PS000801; TRANSKETOLASE_1; 1.
PROSITE; PS000801; TRANSKETOLASE_2; 1.
SEQUENCE 709 AA; 75747 MM; IFBA36ZA0DEDC6D3 CR
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Q9FSG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Narcissus pseudonarcissus (Daffodil).
Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation updat
1-D-desoxyxylulose 5-phosphate synthase (DXS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A cDNA encoding 1-D-desoxyxylulose 5-phosphate synthase Narcissus pseudonarcissus L.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ279019; CAC08458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Schaub P., Beyer F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=39639;
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                                                                                                                  44.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Al-Babili S.;
                                                                                       107;
                                                                                       Score 1435.5; DB 10;
Pred. No. 5.8e-96;
7; Mismatches 195; I
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Q9SP65;
01-MAY-2000
01-CCT-2000
01-CCT-2002
                                                                                                                        STRAIN=cv. Yugoslavia; TISSUB=Root; Wobbe K.K., Souret F.P., Shore K.A., Weathers P.J.; Wobbe K.K., Souret F.P., Shore K.A., Weathers P.J.; Wattemisia annua D-1-deoxyxylulose-5-phosphate synthase Submitted (MAY-2000) to the BMBL/denBank/DDBJ databases. InterPro; IPR005476; Dxs. InterPro; IPR005476; Transketolase CR. InterPro; IPR005475; Transketolase CR. InterPro; IPR005475; Transketolase N. InterPro; IPR005474; Transketolase N. InterPro; IPR005474; Transketolase N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Artemisia annua (Sweet wormwood).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledona; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) 1-deoxy-D-xylulose-5-phosphate synthase.
                                            InterPro, IPR005474, Transketolase

Pfam, P702780, transketolase_C; 1.

Pfam, PF02779; transket_Dyr; 1.

TIGRPAMs; TIGR00204; dxs; 1.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anthemideae; Artemisia.
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diphosphate synthesis.";
FEBS Lett. 460:485-490(1999)
[2]
                                                           *A Synechococcus leopoliensis SAUG 1402-
deoxyxylulose 5-phosphate synthase gene
reading frames is functionally involved
                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=20026086; PubMed=10556522;
Miller B., Heuser T., Zimmer W.;
                                                                                                                                                                                                Bacteria; Cyanobacteria;
NCBI_TaxID=1140;
                                                                                                                                                                                                                                                Synechococcus sp.
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Q8W4V1;
01-MAR-2002 (TrEMBLrel. 20, Cro
01-MAR-2002 (TrEMBLrel. 20, Las
01-MAR-2003 (TrEMBLrel. 23, Las
Deoxy-D-xylulose-5-phosphate s
                  Morinda citrifolia (Indian mulberry).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Gentianales; Rubiaceae; Rubioideae; Morindeae;
                                                            DXS
          Asteridae;
Morinda.
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                                                                                                                                                                                                              KPLDEELIVPLARQIGKVVTPEEGCLPGGFGSAIMESLQAHDLQVPVLPIGVPDLLVEHA
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                                                                                                                                                                       SPDESKQELGLTPROMADRILEKF
                                                                             (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 23, Last annotation updat
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Pred. No. 7.4e-96;
9; Mismatches 209;
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Best Local S
Matches 302
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InterPro; IPR005476; Transketolase_C.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005474; Transketolase_N.
Pfam; PP02780; transketolase_C; 1.
Pfam; PP02779; transketolase_C; 1.
Pfam; PP02779; transket_pyr; 1.
TIGRPAMs; TIGR00204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
SEQUENCE 722 AA; 77970 MW; 58231942EAF9C767 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Han Y.S., Roytrakul S., Verberne M.C., Heijden, R
Han Y.S., Roytrakul S., Verberne M.C., Heijden, R
"Cloning and characterization of a cDNA encoding
phosphate synthase from Morinda citrofolia.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ dat
EMBL; AF443590; AAL32062.1; -.
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VL---MPVCNIGLPDRFVEQGSREELLSLVGLDSKGILATI
:| :::|||:::|| :: || |:| ||:
LLDGPIKLRSMVLPDRYIDHGSPADQIEQAGLSSRHICATV
                                                                                                                                                                                                  MREGSGILVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIH
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                                                                                                                   Q-HHGPASVRYPRGKGPGAAIDPTL--TALEIGKAEVRHHGSRIAILAWGSMVTPAVEAG
                                                                                                                                                                DVALQNIDMIFALDRAGIVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMITTGF
                                                                                                                                                                                                                                                                                                                   VKGMIVP--GTLFEBLGFNYFGFIDGHDVEMLVSTLENLKDL--TGPVFLHVVTKKGKGY
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                                                 KQL-----GATVVNMRFVKPFDQALVLBLARTHDVFVTVBENVIAGGAGSAINTFLQAQK
                                                                                                                                                   DVDLQKLPVRFAMDRAGLVGADGPTHCGAFDVAYMACLSNMIVMAPADEAELMHMVATAA
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                                                                                                   TIDDRPCCFRFPRGNGIGAKLPPDNKGNLIGIGKGRILTEGSRVALIGYGAIVQQCLGAA
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47.1%;
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Pred. No. 1.40
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g 1-deoxy-D-xylulose
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Search completed: January 29, 2004, 15:54:02 Job time : 49.2142 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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1 MKGICILGATGSIGVSTLDV.....LQADQDAREVARDIIKTLVA 394
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Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

RESULT 1

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KOffas M, Odom JM, Schenzle A; WPI; 2002-452200/48.	(DUPO) DU PONT DE NEWOURS & CO E I.	01-SEP-2000; 2000US-229858P.	28-AUG-2001; 2001WO-US26827.	14-MAR-2002.	WO200220728-A2.	Methylomonas 16a.	nitrous oxide; terpenoid; animal feed; carotenoid; exopolysaccharide.	methane-containing environment; waste water treatment system; isoprenoid;	ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill;	pyrophosphate dependent phosphofrutokinase; nitrogen-containing compound;	methane; methanol; Embden-Meyerhof carbon flux pathway; 16s RNA;	High growth methanotrophic bacterial strain; C1 carbon substrate; enzyme;	High growth methanotrophic bacterial strain polypeptide #32.		27-AUG-2002 (first entry)		ABG61582;		ABG61582 standard; Protein; 394 AA.	1582

ABP80486

ABK83261.

functional gene encoding in Embden-Meyerhof carbon pathway high growth methanotrophic bacterial strain, useful for producing ale cell proteins, grows on a Cl carbon substrate, and comprises a

Ś ᅜ S Ş B S 밁 S 멼 181 121 121 241 181 394; 61 61 MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCIAHHPEYAVVVMES VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLT 180 OIEVVIHPOSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGH ASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPD ASGGPFRRTPIBTLSSVTPDQAVAHPKWDMGRKISVDSATWMNKGLELIEACLLFNMEPD VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLT KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGKIDALYEQCLAHHPEYAVVVMES 0 120 180 300 240 60 60

25-JUL-2002 (first

protein and for the biokransformation of a nitrogen-containing compound, ce g. ammonia, nitrate, nitrite or nitrogen. It is also useful for the groduction of a feed product comprising a protein, carbohydrates and a compignment and for reducing oxygen demand, for removing nitrates and nitrites in methane-containing environments such as landfills, waste carbohydrates. The bacterial strain of the invention can be used as a containing agent for the conversion of nitrate or nitrite to nitrous conditions of biomass including proteins, carbohydrates and wide converted of pigments (particularly for isoprenoid pigments for the conversion of nitrate or nitrite and wide conversed for generating animal feeds), in production of terpenoid and carbohed and in production of exopolysaccharides at high levels.

CC materials and in production of exopolysaccharides at high levels.

CC material strain proteins of the invention which grows on a C1 carbon substrate e.g. methane and methanol, and comprises a functional Embden-Meyerhof carbon flux pathway comprising a comprises a functional Embden-Meyerhof bhosphofrutokinase enzyme or a 16s Claim 11; Page 141-142; 157pp; English invention relates to a high growth methanotrophic bacterial strain, the grows on a C1 carbon substrate e.g. methane and methanol, and coding a pyrophosphate dependent phosphofrutokinase enzyme or a The bacterial strain is useful for the production of single cell strain proteins of the invention

Sequence 394 AA;

Query Match Best Local S Matches 394 Similarity 100.0%; ilarity 100.0%; Conservative (Score 1985; DB 23; Pred. No. 1.8e-185; Mismatches Indels Length 394; 0

QIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGH

300

361 MDFEKPDLKRFPCLRLAYEALKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSM AQFKPDDAGSLELVLQADQDAREVARDIIKTLVA 394

Вb Ś ₽,

394

Methylomonas 16a sp. D-1-deoxyxylulose-5-phosphate reductoisomerase

aquaculture; enzyme; D-1-deoxyxylulose-5-phosphate reductoisomerase; Carotenoid; isopentenyl l pyrophosphate; flavour: fragra fragrance; electro-optic antheraxanthin; astaxanthin; diet;

Methylomonas 16a sp.

W0200218617-A2

07-MAR-2002

04-SEP-2001; 2001WO-US27420

01-SEP-2000; 2000US-229858P 2000US-229907P

Brzostowicz PC, Cheng Q Odom JM, Picataggio SK, DUPO) DU PONT DE NEMOURS & CO ю Dicosimo DJ, Rouviere PE; Ħ Koffas M, Miller ES

WPI; 2002-351711/38.

producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon

Claim 42; Page 112-114; 156pp; English

encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carl substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. D-1-deoxyxylulose-5-phosphate reductoisomerase (Dxr) enzyme used in the invention. The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule carbon уď

Sequence 394

Matches Query Match Best Local 394; Similarity Conservative 100.0%; Score 1985; 100.0%; Pred. No. 1.1 tive 0; Mismatches , DB 23; 1.8e-185; 0 Indels Length 0 Gaps 0

S 밁 á 밁 Ş F S 딹 181 121 181 121 61 61 VLLANKEAL VMSGQI FMQAVSDSGAVLLP IDSEHNAI FQCMPAGYTPGHTAKQARRI LLT KVABFKORIAASPVADIKVISGSBALQOVATIENVDTVMAAIVGAAGLIPTLAAAKAGKT QIEVVIHPOSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGH MKGICILGATGSIGVSTLDVVARHÞDKYQVVALTANGNIDÁLYBQCLAHHÞEYAVVVMBS MKGICILGATGSIGVSTLDVVARHDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMBS ASGGPFRTTPIBTLSSVTPDQAVAHPKWDMGRKISVDSATMANKGLELIBACLLFNMEPD VILLANKEAL VMSGQI FMQAVSDSGAVLLP I DSEHNAI FQCMPAGYTPGHTAKQARRILLT KVABFKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 300 120 60 120 60 240 240 180 180

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RESULT 3
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                                                              Query Match
Best Local S
Matches 394
                                                                                                                                                    The present invention relates to a new nucleic acid molecule encoding an isoprenoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an isoprenoid compound biosynthetic enzyme, and for the invention are also useful for regulating isoprenoid biosynthesis in an organism and for producting recombinant organisms for producing various isoprenoid compounds. The molecules of the invention are also useful for regulating isoprenoid biosynthesis in an organism and for producing recombinant organisms for producing various isoprenoid compounds. The mucleic acid is also useful for feed additive, for the production of keratenoids and their derivatives, isoprenoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 2 (ORF2) dxr (1-deoxyxylulose-5-phosphate reductoisomerase enzyme) protein of the invention, as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive; keratenoid; pigment; flavour; fragrance; open reading frame 2; ORF2; dxr; 1-deoxyxylulose-5-phosphate reductoisomerase enzyme.
                                                                                                                           Sequence
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 MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES 60
                                                                                                                                                                                                                                                                                                                                                                                                                         cleic acid molecule encoding a isoprenoid biosynthetic enzyme, from Methylomonas 16a, useful for the production of isoprenoid
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\, Tomb J;
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ilarity 100.0%;
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KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120

Query Match

61

28;

Score

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Length

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396 AA

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RESULT 4
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                                                                                 The invention relates to methods and materials for the production of isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS) activity or decaprenyl diphosphate synthase (DXS) activity, is useful for increasing production of CoQ(10) in a cell having endogenous DDS activity. This sequence represents a protein relating to the isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity,
                                                             production
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 32; 246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             production of isoprenoids, especially CoQ(10)
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Matches
The invention relates to methods and materials for the production of isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS)
                                                                                                                                                                                                                                              Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                                                                                                                                             Disclosure; Fig 32; 246pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; DXS;
decaprenyl diphosphate synthase.
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Escherichia coli
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29-SEP-2000; 2000US-236580P

(CRGI) CARGILL INC

Gokarn 'n Jessen H, Zidwick

WPI; 2002-416480/44

Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10) useful for the

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Matches 219; Conserval
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                                                                                                         04-APR-2002
                                                                                                                                                                                                                                                                                                      AA021885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure
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                                                                                                                                    W0200226933-A2
                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                              Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; decaprenyl diphosphate synthase.
                                                                                                                                                                                                                                           Isoprenoid related protein sequence
                                                                                                                                                                                                                                                                         13-SEP-2002
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                 CARGILL
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                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                             NLSVLEKMDMREPQCVDDVLSVDANAREVARKEVMRLAS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CKLSALTFAAPDYDRYPCLKLAMEAFEQGQAATTALNAANEITVAAFLAQQIRFTDIAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NASASQMEVLTHPQSVTHSMVRYQDGSVLAQLGEPDMRTPTAHTMAWPNRVNSGVKPLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILLIGSGGPFRETPLRDLATMIPDQACRHPNWSMGRKISVDSATWMNKGLEYIEARWLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILLANKESLYTCGRLFMDAVKQSKAQLLFVDSEHNAIFQSLFQPIQHNLGYADLEQNGVV 179
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Pred. No. 2e-93;
56; Mismatches 118;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                                                            N. gonorrhoeae
                                                                                                                                         07-MAR-2003
                                                                                                                                                                    ABP79699;
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                                                    Neisseria gonorrhoeae
                                                                                   Antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                standard;
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Pred. No. 2e-93;
6; Mismatches 118;
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins an antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP75736-ABP81046 represent nucleic acid molecules of the invention.
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               Antibacterial;
                                                                   07-MAR-2003
                                                                                            ABP80486;
                                                                                                                     ABP80486 standard;
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                                        gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein from Neisseria gonorrheae, cament for treating or preventing
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                                                                                                                                                                                                            KPDDAGSLELVLQADQDAREVARDIIKTL
                                                                                                                                                                                                                                     QKPDFGRFPCLKFAYETINAGGAAPCVLNAANETAVAAFLDGQIKFTDIAKTVAHCLAQD 381
                                                                                                                                                                                                                                                              EKPDLKREPCIRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKETDIAVIIERSMAQF 363
                                                                                                                                                                                                                                                                                           VVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIÄYCLGLPERIDSGVGKIDFGALSALTF 321
                                                                                                                                                                                                                                                                                                         VVIHPQSIIHSMYDJYDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGHMDF
                                                                                                                                                                                                                                                                                                                                              GPFLTTDLSTFDSITPEQAVKHPNWRMGRKISVDSATMANKGLELIEAHWLFNCPPDKLE
                                                                                                                                                                                                                                                                                                                                                                     GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPDQIE 243
                                                                                                                                                                                                                                                                                                                                                                                                ANKETLYVSGALFMETARANGAAVLPVDSEHNAIFQVLPRDYTDRLNEHGIDSIILTASG
                                                                                                                                                                                    FSNGMGDIEGLLAQDARTRAQARAFIGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 AA;
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               infection; vaccine;
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Pred. No. 3e-93
48; Mismatches
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RESULT 10
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New protein from Neisseria gonorrheae, medicament for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 734; 815pp;
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                                                                                                    VVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAYCLGLPERIDSGVGKLDFGALSALTF
                                                                                                                                 VVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTFIAHAMAWPERFDSGVAPLDIFEVGHMDF
                                                                                                                                                                                    GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPDQIE
                                                                                                                                                                                                                ANKETLYVSGALFMETARANGAAVLPVDSEHNAIFQVLPRDYTDRLNEHGIDSIILTASG
                                                                                                                                                                                                                                                                      RIEALLKROGTA-TQVLHGAQALVDVASADEVSGVMCAIVGAAGLPSALAAAQKGKTIYL
                                                                                                                                                                                                                                                                                             EFKQRIAASEVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLETLAAAKAGKTVLL
                                                                                                                                                                                                                                                                                                                                                 ICILGATGSIGVSTLDVVARHPDXYQVVALTANGNIDALYEQCLAHHPEYAVVVMESKVA
                                                   QKPDFGRFPCLKFAYETINAGGAAPCVLNAANETAVAAFLDGQIKFTDIAKTVAHCLAQD
                                                                            EKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSMAQF
                                                                                                                                                          GPFLTTDLSTFDSITPEQAVKHPNWRMGRKISVDSATMANKGLELIEAHWLFNCPPDKLE
                                                                                                                                                                                                                                         ANKEAL VMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG
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 FSNGMGDIEGLLAQDARTRAQARAFIGTL 410
                        KPDDAGSLELVLQADQDAREVARDIIKTL 392
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Pred. No. 3e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
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                                                                                                                      FNMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAMPERFDSGVAPLD
                                                                                                                                                       SKIVLTGSGGPFRYTPLEQFEQITPAQAVAHPNWSMGKKISVDSATMMNKGLEYIEARWL
                                                                                                                                                                       RRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMUKGLELIEACLL
                                                                                                                                                                                                                                                                                       KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAALVGAAGLLPTLAAAKAGKT 120
                                                                                                                                                                                                                                                                                                                  MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES 60
LNCLVVSKLQPQKIHCIEDVLEVDKKARELSQSII
                      IIERSMAQFKPDDAGSLELVLQADQDAREVARDII
                                                                          I FEVGHMDFEKPDLKRFFCLRLAYEAIKSGGIMFTVLNAANEIAVEAFLNBEVKFTDIAV 354
                                                                                                                                                                                                             VILLANKEALVTCGQLFIDAVRESQAQLLPVDSEHNAIFQSLPPEAQRQIGFCP-LSELGI 179
                                                                                                                                                                                                                                                                 AAKMLAEKLKAHQ-SQTTVLAGQQAICELAAHPEADMVMAAIVGAAGLLPTLSAVKAGKR
                                                   FYQLNGLTFIEPDYQRYPCLKLAIDAFSAGQYATTAMNAANEIAVASFLDNKIKFTDIAR
                                                                                                      FNASAEEMEVIIHPQSIIHSMVRYIDGSVIAQMGNPDMRTPIAETMAYPSRTVAGVEPLD
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Pred. No. 4.1e-93;
58; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                                                                                                                                                                                                                                                                                    Sequence
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NASAEEMEVIIHPOSIIHSMVRYVDGSVITOMGNPDMRTPIAETMAYPHRTFAGVEPLDF
                                                                       LLANKBALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMP-----AGYTPGHTAKQAR 175
                                                                                                                                                                AKILREKLIAHHI-PTEVLAGRRAICELAAHPDADQIMASIVGAAGLLPTLSAVKAGKRV
                                                                                                                                                                                                                      QNIVILGSTGSIGKSTLSVIENNPQKYHAFALVGGKNVEAMFEQCIKFRPHFAALDDVNA
                                                                                                                                                                                                                                                 KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK
              NMEPDQIEVVIHPQSIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDI
                                                     KIILTGSGGPFRYTPLEQFTNITPEQAVAHPNWSMGKKISVDSATYMNKGLEYIEARWLF
                                                                                                                                                                                           VARFKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTV
                                                                                                           LLANKESLVTCGOLFIDAVKNYGSKLLFVDSEHNAIFQSLFPEAQEKIGFCF-LSELGVS
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Pred. No. 1.1e
76; Mismatches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, useful production of isoprenoids, especially CoQ(10) -
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decaprenyl diphosphate synthase.
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LLANKESLYTCGQLFIDAVKNYGSKLLPVDSEHNAIFQSLPPEAQEKIGFCP-LSELGVS
                                                                                                              AKILREKLIÄHHI-PTEVLAGRRÄICELÄÄHPDADQIMASIVGAAGLIPTLSAVKAGKRV
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                                                    LLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMP-----AGYTPGHTAKQAR
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Pred. No. 1.1e-89;
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                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                        pleural
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Modulating Haemophilus influenzae DXR reductoisomerase enzyme activity, useful for treating mammals or tissues infected with H. influenzae (e.g. ear infections or pneumonia) by contacting the enzyme with a modulator of its activity -

Claim 6(i); Page 5; 44pp; English.

The invention relates to modulating an activity of a DXR reductoisomerase enzyme of Haemophilus influenzae, comprising contacting the enzyme with a compound that modulates non-mevalonate isoprenoid biosynthesis - synthesis of menaquinone or ubiquinone. Compounds of the invention act as virucides. The method is useful for treating a mammal or mammalian tissue infected with H. influenzae having DXR reductoisomerase enzyme, e.g. a human or a domestic animal. In particular, the method is useful for treating ear infections, conjunctivitis, meningitis, pneumonia, conjunctivitis, bacteraemia, sinusitis, pleural empyema, endocardicis and epiglottitis. The current sequence represents the H. influenzae DXR reductoisomerase anzyme of treating earnesses. reductoisomerase enzyme polypeptide sequence.

Note: In the sequence listing, on page 40-44 of the specification, is given an amino acid sequence that is also described as SEQ ID 2, is the identifier of the current sequence. This sequence is given i record ABB09437, and contains the amino acids given in the current sequence but with a large insertion of extra amino acids that are resequence but with a large insertion of extra amino acids that are resequence but with a large insertion of extra amino acids that are resequence. are not which

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          Disclosure; Fig 27; 246pp; English
                                               Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity,
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                                                                                                                                                                                                                                                             Zymonas mobilis.
                                                                                                                                                                                                                                                                                   Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase;
decaprenyl diphosphate synthase.
                                                                                                                                                                                                                                                                                                                      Isoprenoid related protein sequence SEQ ID No 101
                                                                                                                                                                                                                                                                                                                                                                          AA021879;
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                                   production of isoprenoids, especially CoQ(10)
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Pred. No. 1.1e-89;
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ilarity 50.9%;
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XX WO200
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PR 28-SE
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AA021883
standard;
Protein;
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13-SEP-2002
(first entry)
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Isoprenoid related protein sequence SEQ ID No 116.

decaprenyl diphosphate synthase. Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; DXS; DDS;

Zymonas mobilis

WO200226933-A2

04-APR-2002

28-SEP-2001; 2001WO-US30328

29-SEP-2000; 2000US-236580P

(CRGI) CARGILL INC

Gokarn Þ Jessen H, Zidwick MJ;

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TPATPSSLEDVFAIDNEARIQAAALMESLPA
                                  KPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                                                                                 EKPDIKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFINEEVKFTDIAVIIERSMAQF 363
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US-08-426-819A-36
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US-09-491-362-2
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741 620 111 107 105.5

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Sequence 7, Application US/09491362

Patent No. 6281017

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Lange, Bernd M

TITLE OF INVENTION: L-DBOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND

TITLE OF INVENTION: METHODS OF USE

FILE REFERENCE: WSUR14977

CURRENT APPLICATION NUMBER: US/09/491,362

CURRENT FILING DATE: 2000-01-26

EARLIER APPLICATION NUMBER: 60/118,349

EARLIER FILING DATE: 1999-02-03

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Ver. 2.0

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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMAUNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7199

LENGTH: 398

TYPE: No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Acinetobacter baumannii
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                                                                                                                                                                                                                                                                                                                                                                 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNM 237
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                                                                                                                                                                                                                                                                                                                                                                 HTLEKLENAAAESIECILDKDKVARSVAQQYISSI 396
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                    ; LENGTH: 399
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-874-562-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09874562 Patent No. 6420159 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 13
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APPLICANT: Lange, Bernd
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Query Match 41.2%; Score 818.5; DB 4; Best Local Similarity 44.6%; Pred. No. 1.6e-81; Matches 176; Conservative 71; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lange Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR17549
CURRENT APPLICATION NUMBER: US/09/874,562
CURRENT FILLING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR APPLICATION NUMBER: 09/418,349
PRIOR PILLING DATE: 1909-02-03
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                                                            62 VABPKORIĄASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLIPTLAAAKAGKTV 121
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INELKEALADLDY-KLBIIPGEQGVIEVARHPEAVTVVTGIVGCAGLKPTVAAIEAGKDI 121
                                                                                                                                                                                           KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK 61
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44.6%; Pred. No. 1.6e-81;
tive 71; Mismatches 131;
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APPLICANT: Busch, Marco
APPLICANT: Hain, Rudiger
APPLICANT: Marcin, William
APPLICANT: Tietjen, Klaus
APPLICANT: Kloti, Andreas
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US-09-449-335-6
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Patent No. 6303365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Method of determining the activity of TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate reductoisomerase TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate synthase FILE REFERENCE: 2020US

CURRENT APPLICATION NUMBER: US/09/449,335

CURRENT FILING DATE: 1999-11-24

EARLIER APPLICATION NUMBER: DE 199 35 967.9

EARLIER FILING DATE: 1999-07-30

NUMBER OF SEQ ID NOS: 8

SOFTMARE: Patentin Ver. 2.1
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FEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVI
                                        YDDIEIVIHPQSIIHSMIETQDSSVLAQLGWPDMRLPILYTMSWPDRVPCSEVTWPRLDL
                                                                           PDQIEVVIHEQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAP---LDI
                                                                                                                   LTASGGAFRDWPVEKLKEVKVADALKHPNWNWGKKITVDSATLFNKGLEVIEAHYLFGAE
                                                                                                                                                       LTASGGPERRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLENME
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US-09-449-335-2
GENERAL INFORMATION:
APPLICANT: Busch, Marco
APPLICANT: Hain, Rudiger
APPLICANT: Martin, William
APPLICANT: Tietjen, Klaus
APPLICANT: Alotti, Andreas
ITITLE OF INVENTION: Method o
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US-09-480-921B-10
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CURRENT FILING DATE: 2000-01-11
NUMBER OF SEO ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 477
TYPE: PRT
                                                                                                                   sequence 2, Application US/09449335
Patent No. 6303365
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Best Local Similarity
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APPLICANT: Budziszewski, Gregory J.
APPLICANT: Potter, Sharon L.
APPLICANT: Wegrich, Lynette M.
TITLE OF INVENTION: Herbicide Target Genes and
FILE REFERENCE: PB/5-30780A
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44.6%; Pred. No. 2.8e-81;
tive 69; Mismatches 127;
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APPLICANT: Potter, Sharon L.

APPLICANT: Wegritch, Lymette M.

TITLE OF INVENTION: Herbicide Target Genes an

FILE REFERENCE: PB/5-30780A

CURRENT APPLICATION NUMBER: US/09/480,921B

CURRENT FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/09480921B Patent No. 6387637 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.0%; Score 814.5; DB 4; Best Local Similarity 44.3%; Pred. No. 6.1e-81; Matches 175; Conservative 71; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Arabidopsis thaliana
-09-449-335-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/449,335
CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: DE 199 35 967.9
EARLIER FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Levin, Joshua Z. APPLICANT: Budziszewski, G
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OTHER INFORMATION:
NAME/KEY: SITE
                                             NAME/KEY: SITE LOCATION: (39)
                                                                                                            TYPE: PRT
ORGANISM: Arabidopsis
                                                                                             EATURE:
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Matches

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RESULT 9
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Best Local S
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                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Appli
Patent No. 628101
                                   Query Match
                                                                                                                                                      CURRENT FILING DATE: 2000-01-26
EARLIER APPLICATION NUMBER: 60/118,349
EARLIER FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                               APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR14977
                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/491,362
                                                                                   LENGTH: 475
TYPE: PRT
ORGANISM: Mentha piperita
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: SITE
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   Local Similarity hes 172; Conserv
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37.3%; Score 741; DB 3; Length 47 ilarity 43.0%; Pred. No. 7.8e-73; Conservative 73; Mismatches 133; Indels
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                                   Length 475;
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CURRENT APPLICATION NUMBER: US/09/874,562
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 09/491,362
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/118,349
PRIOR FILING DATE: 1999-02-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 2
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US-09-874-562-2
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APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
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                                                                                                                                                                                                                                                                                                                                                                                                                                  h 37.3%; Score 741; DB 4; Length 475; Similarity 43.0%; Pred. No. 7.8e-73;
                                                                                                                                                                                                                                                                     VABFKQRIAASPVADI-KVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
MEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMANPDMRTPIAHAMAWPER-PDSGVA--PL
                                                                                                          LLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATM-MNKGLELIBACLLFN 236
                                                                                                                                                                                                                                                                                                                       KPISVIGSTGSIGTQTLDIVAENPDKFRIVALAAGSNVTLLADQ-KAFKPKLVSVKDESL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLLANKBALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQC---MPAGYTPGHTAKQARRI 177
                                                                                                                                                                                                                                          ISELKEALAG--FEDMPEIIPGEQGMIEVARHPDAVTVVTGIVGCAGLKPTVÄAIEÄGKD
                                                                  ILTASGGARDLPVEKLKEVKVADALKHSNWNWGKKNTVRLLQLFFNKGLEVIKAHYLFG
                                                                                                                                                      IALANKETLIAGGPFVLPLAKKHNVKILPADSEHSAIFQCIQGLPEG------ALRRI
                                                                                                                                                                                                                                                                                                                                                                   KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYBQCLAHHPEYAVVVMESK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVVELTCDKHRSEMAVSPSLEEIVHYDQWARDYAATVLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIIERSMAQFKPDDA--GSLELVLQADQDAREVARDIIKT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLCKV-DLPFKKPDNRBIPAMDLAYAAWKSRSTWIGVLSAANEKAVEMPIDEKIGYLDIF 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEYDDIEIVIHSPSIIHSMVETQDSSVLAQLGWPDMRLPILYTLSWPERVYCSEITWPRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILTASGGAFRDLPVEKLKEVKVADALKHSNWNMGKKNTVRLLQLFFNKGLEVIKAHYLFG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATM-MNKGLELIEACLLFN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISELKEALAG -- FEDMPEIIPGEOGMIEVARHPDAVTVVTGIVGCAGLKPTVAAIEAGKD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VABEKORIAAS PVADI-KVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPISVIGSTGSIGTQTLDIVAENPDKFRIVALAAGSNVTLLADQ-KAFKPKLVSVKDESL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TALANKETLIAGGPFVLFLAKKHNVKILPADSEHSAIFQCIQGLPEG------ALRRI
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            73; Mismatches 133; Indels
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US-09-252-991A-31862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 362
LENGTH: 340
                                                                                                                                                                                                                 Sequence 31862, Application US/09252991A Patent No. 6551795
                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 362, Application Patent No. 6559294
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
EILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
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                                                                                                                                                                                                                                                                                                                                                                                                                                  234 APERFASPROGMOFSKKOTLEFFFVDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 IVGAAGLLPTLAAAKAGKTVLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCM 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 IFOQLQEFAPLAAAVYNEEVYNEACQRF----PHMQFFLGQEGLTQLCIMDTVTTVVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNKGLEIIEAYWLFGLENVEILAVIHPQSLIHGWVEFLDGSVISIMNPPDMLFPIQYALT
                                                                                                                                                                                                                                                                                                                                                PLCEEISWCDILRKLTTLMBCHKVYACHSLEDILBVDGEARALAQBI
                                                                                                                                                                                                                                                                                                                                                                                       FINEEVKFTDIAVIIERSMAQFKPDDAGSLELVLQADQDAREVARDI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPERFDSGVAPLDIFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MNKGLELIEACLLFNMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAGYTPGHTAKQARRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSGIEALPAILESMKKGKALALANKEILVCAGELVSKTAKENGIKVLPIDSEHNALYQCL
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                                                                                                                                    D SEQUENCES RELAT AND THERAPEUTICS
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US-09-252-991A-17790
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Best Local S
Matches 85
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILS REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 17790

LENGTH: 2895

TYPE: NET
                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17790, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS:
SEQ ID NO 31862
LENGTH: 671
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
-09-252-991A-17790
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                           y Match 5.4%; Score 107; DB 4; Length 2285; Local Similarity 22.8%; Pred. No. 0.11; hes 87; Conservative 51; Mismatches 137; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 5.6%; Score 111; DB 4; Length 671;
Local Similarity 21.1%; Pred. No. 0.005;
hes 85; Conservative 58; Mismatches 139; Indels 1
                                                                                            1505 LIGAT---FVELLWRLAEHPDEAADFAFLAPRR-DA-----ASQPEPLVDV----VSLF 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 VGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAV 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620 LGEFDRYPPERQQ-----AIETVE-GDVGVLHARAANRVAV 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 GPIDADAGQRLVVGALGHQVDGAADAAAGGNP------AEQGVWSLEHPHA 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 TPDQAVA-HPKW-----DMGRKISVDSATMMNKGLELIEACLLFNMEPDQIEV-----VI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 LVQVGIAQAEACLRVRGWGDVGGSRAGQQRAHHAFQAFLLVQQVAG------QAQALA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 ------QCM------PAGYTPGHTAKQARRILLTASGGPFRRTPIETLSSV 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 AGEVRORRMRRGLVEVARLHPGEGIDHAQPFVQAVGAERPVVAERAGVEVAAQADLGGIG 411
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                                           66 KQRIAASPVADIKVLSGSEAL---QQVATLENVDTVMAAIVGAAGLLFTLAAAKAGKTVL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 VAEFKORIAASPVADIKVLSGSEALQQ------VATLENVDTVMAAIVGAAG 107
                                                                                                                                             6 ILGATGSIGVSTLDVVARHPDKXQVVALTANGNIDALYEQCLAHHPEYAVVVMESKVAEF 65
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184	149PIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG 183 	2IVGAAGLLPTLAAAKAGKTVLLANKEALVMSGQIFMQAVSDSGAVLL 14 	62 VARFKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAA	2 KGICILGAFGSÍGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK 61 :	ry Match 5.3%; Score 105.5; DB 3; Length 3816; t Local Similarity 17.8%; Pred. No. 0.41; ches 98; Conservative 76; Mismatches 151; Indels 227; Gaps 25;	LENGTH: 3816 TYPE: PRT ORGANISM: Artificial Sequence FRANTURE: FRANTURE: OTHER INFORMATION: Description of Artificial Sequence: Recombinant OTHER INFORMATION: Oleandolide PKS 9-428-517-3	RAIBER FILING DATE: 1998-10-29 HBER OF SEO ID NOS: 12 TTWARE: Patentin Ver. 2.1 ID NO 3	FILING DATE: 1999-10-28 APPLICATION NUMBER: 60/120,254 FILING DATE: 1999-02-16 ADDLICATION NUMBER: 60/106 106	APPLICANI: THIG, LI TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 30062-20029.00 CHERENT APPLICATION NUMBER: US/09/428.517	Shah, McDan:	ce 3, Application US No. 6251636 L INFORMATION:	14 428-517-3	1797 PGALRVVVSSGEQLRITEDVR 1817	328 PTVLNAANEIAVEAPINEBVK 348		בריך אונסטקאר (מיזיסט בריך מא זחמאפטער אינט אינט אינט אינט אינט בריך פרופסיםטער אינט אינט אינט אינט אינט אינט א	227 ELIEACILENMEPDQIEVVIHPQSIIHSM-VDYVDGSVLAQMGNDDNRTPIAHAMA 281	1640 AQPERVVAHPEHAHVAAAERVIEVEELVADIKPETFÄAPOLDELAMLLETSGSTGRPKGV 1699	183 GGPERRTPIETLSSVTPDQAVAHPKWD-MGRKISVDSATWMNKGL 226	1599 VALNRSPENIATIWGILRAGIVCVPLDVSYPA	LANKEALVASGQIEMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTAS 182	1551 ERQVEALPGSAALAFEEQRWTYRDLDHVARCVATRLVRAGARRGDAIG 1598

	90 VAPLDIFEVGHMDPEKPDLKRFPCLRLAYEAIKSGGIMPTVLMAANEI	₽ <i>V</i> 2 €
	128 ALVMSQQIFMQAYSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAXQARRILLTASGGPFR 187	B 6 B 6
	/ Match 5.0%; Score 99; DB 4; Length 482; Local Similarity 20.3%; Pred. No. 9.059; les 86; Conservative 57; Mismatches 156; Indels 124; Gaps 18 20 VVARHPDKYQVVALTANG-NIDALYEQCIAHHPEYAVVNESKVAEPKQRI 69	Query M Best Lo Matches Qy Db Db
PSEUDOMONAS	5 2-991A-20932 2-991A-20932 2-991A-20932 NO. 6551795 L INFORMATION: CANT: MARC J. Rubenfield et al. OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS REFERENCE: 107196.136 NT APPLICATION NUMBER: US/09/252,991A NT FILING DATE: 1999-02-18 APPLICATION NUMBER: US 60/074,788 FILING DATE: 1998-07-18 APPLICATION NUMBER: US 60/094,190 FILING DATE: 1998-07-27 NO 20932 NO 20932 NO 20932 NO 20932 NO PSEQ ID NOS: 33142 NO 20932 NO PSEQ ID NOS: 33142 NO 20932 NO PSEQ ID NOS: 33142 NO PSEQ PSEQ NOS: 33142 NO 20932	RESULT 15 US-09-252- US-09-252- US-09-252- US-09-252- US-09-252-
1 ₽ 1	333AANEIAVEAFLNEEVKFTDIAVIIERSMAQFKPDDAGSLELVLQADQDAR	P & P &
	3366 VARHLUTEHDVRRILLIVSRSGVAPDLAAELGALGAEVTVAACDVANKKALKALLEDIP 3423 228	8 8 8 8 8 8

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1: /cgm2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgm2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgm2 6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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US-09-934-868-64
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Sequence 4, Appli
Sequence 64, Appli
Sequence 8, Appli
Sequence 117, App
Sequence 119, App
Sequence 119, App
Sequence 118, App
Sequence 112, App
Sequence 120, Appl
Sequence 111, App
Sequence 111, App
Sequence 97, Appl
Sequence 97, Appl
Sequence 113, App
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Z-Z	Match Local Simi les 394;	SULT 1 Sequence 4, Applicat patent No. US2002010 GENERAL INFORMATION: APPLICANT: Koffas, I APPLICANT: Schenzi No. US2 APPLICANT: Schenzi No. US2 APPLICANT: Tomb, J APPLICANT: No. US2 APPLICANT: No. US2 APPLICANT: Picatag APPLICANT: Cheng, I Cheng, I TILE OF INVENTION CHENG, I TILING DATE PRIOR APPLICATION OF SEQ ID NO SOFTWARE: MICROSOFT NO SOFTWARE: MICROSOFT SEQ ID NO SOFTWARE: MICROSOFT SEQ ID NO SOFTWARE: MICROSOFT SEQ ID NO 4 LENGTH: 394 TYPE: PRI ORGANISM: Methylom FEATURE: OTHER INFORMATION: OPHER INFORMATION:		886 818.5 818.5 818.5 818.5 817.5 813.5 7798.5 7799.5 7799.5 7799.5 691.5 691.6 691.
KGICILGA KGICILGA	nilarity Conservat	equence 4, Application US/09934903 atent No. US20020102690A1 ENERAL INFORMATION: APPLICANT: Koffas, Mattheos APPLICANT: Schenzle, Andreas J. APPLICANT: No. US20020102690A1ton, APPLICANT: No. US20020102690A1ton, APPLICANT: No. US20020102690A1ton, APPLICANT: No. US20020102690A1ton, APPLICANT: Rouviere, Pierre APPLICANT: Cheng, Qiong TITLE OF INVENTION: Genes Involved i FILE REFERENCE: C11646 US NA CURRENT APPLICATION NUMBER: US/09/93 CURRENT APPLICATION NUMBER: 05/29,907 PRIOR FILING DATE: September 1, 2001 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Microsoft Office 97 BQ ID NO 4 LENGTH: 394 TYPE: PRT ORGANISM: Methylomonas 16a FRATURE: OTHER INFORMATION: Amino acid seque 09-934-903-4		0.000000000000000000000000000000000000
TGSIGVS	100. 100. vative	ication US/09934: 20102690A1 ION: as, Mattheos n, J. Martin nuzle, Andreas J US20020102690A1 JUS20020102690A1 JUS20020102690A1 JUS20020102690A1 JUS20020102690A1 JUS20020102690A1 JUS20020590A1 JUS200		4002 4477 4477 4477 388 388 388 388 477 477 487 487 487 487 487 487 487 4
	88	15/09934 10 acid		112 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES	Score 1985; DB 10 pred. No. 7.2e-186 0; Mismatches 0;	09934903 s eas J. 690Alton, Kelley C. ncois re ephen Involved in Isoprenoid Compounds NA 1.05/09/934,903 -08-22 60/229,907 er 1, 2001 97 a acid sequences encoded by ORF2	ALIGNMENTS	US-10-381-779-102 US-10-381-779-123 US-09-987-025-2 US-09-987-025-2 US-10-381-779-128 US-10-381-779-128 US-10-381-779-129 US-10-381-779-129 US-10-381-779-124 US-10-381-779-124 US-10-381-779-124 US-10-381-779-126 US-10-381-779-127 US-10-381-779-126 US-10-381-779-127 US-10-381-779-126 US-10-381-779-127 US-10-381-779-126 US-10-381-779-127 US-10-381-779-126 US-10-381-779-127 US-10-381-779-126 US-10-381-779-127 US-10-381-779-127 US-10-381-779-127 US-10-381-779-126 US-10-381-779-127 US-10-381-779-127 US-10-381-779-127 US-10-381-779-127 US-10-381-779-130 US-10-381-779-130 US-09-925-778-2 US-10-381-779-130 US-10-156-761-12156 US-10-156-761-12156 US-10-156-761-10436 US-10-156-761-10436
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KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120

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APPLICANT: KOÉFAS, Mattheos

APPLICANT: Odom, James M

FILE REFERENCE: CL1596 US NA

CURRENT APPLICATION: DENITRITYING METHANOTROPHIC BACTERIAL STR

FILE REFERENCE: C11596 US NA

CURRENT APPLICATION NUMBER: US/09/934,868

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Microsoft Office 97

SEQ ID NO 64

LEINGTH: 394

TYPE: PRI

ORGANISM: Methylomonas 16a

FEATURE:

OTHER INFORMATION: Amino Acid semigross encoded by DXR

FEATURE:
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Best Local Similarity 100.
Conservative
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                                                                                                                                                                                                                                   VLLANKEALVMSGQIFMQAVSDSGAVLLFIDSEHNAIFQCMPAGYTFGHTAKQARRILLT
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              MDFEKPOLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSM 360
                                                                                         QIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGH
                                                                                                                                 ASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATWMNKGLELIEACLLFNMEPD
                                                                                                                                                                    ASGGPPRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPD
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LENGTH: 394
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APPLICANT: Cheng, Qiong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/229,907
PRIOR PILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
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CURRENT FILING DATE: 2001-09-0
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APPLICANT: Miller, Edward S. Jr.
APPLICANT: Odom, J. Martin
APPLICANT: Picataggio, Steve
APPLICANT: Rouviere, Pierre E.
APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: CARCTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Methylomonas 16a
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                                                                                                     MDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSM 360
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                 AQEKPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                                                                                                           QIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPLAHAMAMPERFDSGVAPLDIFEVGH
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AQEKPDDAGSLELVLQADQDAREVARDIIKTLVA
                                                                      MDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANBIAVEAFLNEEVKFTDIAVIIERSM
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DiCosimo, Deana J.
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394
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RESULT 4 US-10-381-779-117 ; Sequence 117, A)

Application US/10381779

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APPLICANT: Gorario, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Jedwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 117
LENGTH: 396
                APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Wary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOTTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Pseudomonas aeruginosa
US-10-381-779-117
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Best Local Similarity 64...
245; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 119, Application US/10381779 Publication No. US20030219798A1
SEQ ID
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APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Sidwick, Mary Jo
TITLB OF INVENTION: Isoprenoid Production
FILLS REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-09-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 100
LENGTH: 398
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; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-381-779-119
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                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-381-779-100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 100, Application US/10381779 Publication No. US20030219798A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 216; Conserv
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Best Local Similarity
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                                                                                                                                                                219;
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61 S-AKILKTMIQQQGSRTEVISGQQAACDWAALEDVDQVWAAIVGAAGLIPTIAAIRAGKT
                                      61 KVABFKORIAASPVADIKVLSGSBALQOVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
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                                                                                                        1 MKGICILGATGSIGVSTLDVVARHDDXYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
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                                                                                                                                                                Conservative
                                                                                                                                                                                 52.6%; Score 1045; DB 12; 54.9%; Pred. No. 1.1e-93;
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                                                                                                                                                              56; Mismatches 118;
                                                                                                                                                                                                     Length
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US-10-381-779-118
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Best Local Similarity 54.9%;
Matches 219; Conservative 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 118
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Escherichia coli
-10-381-779-118
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
FILE REFERENCE: 12904/002US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                  296 FEVGHMDFEKPDIKRFPCIRLAYEAIKSGGIMPTVLNAANBIAVZAFILNEEVKFTDIAVI 355
                                                                                                                                                         180 SILLIGSGGPFRETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIEARWLF
                                                                                                                                                                                  176 RILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATWMNKGLELIEACLLF
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                                                                                                                                                                                                                                                                                                               61 S-AKLLKTMLQQQGSRTEVLSGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKT
                                                                                                                                                                                                                                                                                                                                  KVASFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLFTLAAAKAGKT 120
                                                                                                    NWEPDQIEVVIHPQSIHSMVDYVDGSVLAQWGNPDWRTPIAHAMAMPERFDSGVAPLDI 295
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    CKLSALTFAAFDYDRYPCIKLAMEAFEQGQAATTALNAANEITVAAFLAQQIRFTDIAAL
                                                                              NASASQMEVLIHEQSVIHSMVRYQDGSVLAQLGEPDMRTPIAHTMAWENRVNSGVKPLDF
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o. US20030219798A1
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                                                                                              Sequence 99, Application US/10381779
Publication No. US20030219798A1
GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
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CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: CT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 122
LENGTH: 405
TYPE: PRT
ORGANISM: Pasteurella multocida
US-10-381-779-122
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APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
FILE REFERENCE: 12904/002US1
                                                                355 IIERSMAQFKPDDAGSLELVLQADQDAREVARDII 389
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LNQLVVSKLQPQKIHCIEDVLEVDKKARELSQSII 399
                                                                                                                          FYQLNGLTFIEPDYQRYPCLKLAIDAFSAGQYATTAMKAANEIAVASFLDNKIKFTDIAR
                                                                                                                                                                                           IFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLMAANEIAVEAFLNEEVKFTDIAV 354
                                                                                                                                                                                                                                                            FNASABEMEVTIHPQSIIHSMVRYIDGSVIAQMGNPDMRTFIABTMAYPSRTVAGVEPLD
                                                                                                                                                                                                                                                                                                 FNMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTFIAHAMAWPERFDSGVAPLD
                                                                                                                                                                                                                                                                                                                                                                                             SKÍVLTGSGGÞERYTÞLEQFEQITÞAQAVÁHÞNWSMGKKISVDSÁTMMNKGLEYIEÁRWL 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKKIVILGSTGSIGTSTLSVITHNPDKYQVFALVGGRNVELMFQQCLTFQPSFAALDDDV 66
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120
LENGTH: 397
                                                 ; LENGTH: 397
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-381-779-120
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; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-381-779-99
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US-10-381-779-120
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LENGTH: 397
Query Match
Best Local Similarity
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PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOPTWARDS: 5------
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CURRENT FILING DATE: 2003-03-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLF 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEVGHMDPEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNBEVKFTDIAVI
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50.7%;
Score 1007; DB 12; Pred. No. 6e-90;
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RESULT 11
US-10-381-779-101
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 199
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Publication No. US20030219798A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zymonas mobilis
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184 GPFRRTPIETLSSYTPDQAVAHPKWDMGRKISVDSATMYNKGLELIEACLLFNWEPDQIE
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                                                                                                                                                                                                       EFKORIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTVLL 123
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                                                                                                ANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG 183
                                                                                                                                                                                                                                                     VTVLGATGSIGHSTLDLIERNLDRYQVIALTANRNVKDLADAAKRTNAKRAVIADPSLYN 66
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                                                                                                                                                                                                                                                                                                                                         50.4%; Score 999.5; DB 1
50.9%; Pred. No. 3.2e-89;
tive 74; Mismatches 109
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                                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 388;
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US-10-381-779-116
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 116
LENGTH: 388
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Publication No. US20030219798A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ORGANISM: Zymononas
-10-381-779-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
FILE REFERENCE: 12904/002US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 50.4%;
Local Similarity 50.9%;
  358
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                                                                                                                                                                                         VVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAMPERFDSGVAPLDIFEVGHMDF 303
                                                                                                                                                                                                                                                                                                                             ANXESTVSAGGEMIDAVREHGTTLLPVDSEHNAIFQCF----PHHNRDYVRRIIITASG
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TPATPSSLEDVFAIDNEARIQAAALMESLPA 388
                                       KPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                                                                                                                                                                                                                                                     GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMANKGLELIEACLLFNMEPDQIE 243
                                                                                                                                                                                                                                                                                                                                                                       ANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG 183
                                                                                                                                                                                                                                                                                                                                                                                                                DLKEALAGS----SVEAAAGADALVEAAMM-GADWIMAAIIGCAGLKATLAAIRKGKTVAL 122
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                                                                                 EAPDYERFPALTLAMESIKSGGARPAVMNAANEIAVAAFLDKKIGFLDIAKIVEKTLDHY 357
                                                                                                                    EKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSMAQF 363
                                                                                                                                                              ILVHPQSVIHSMVEYLDGSILAQIGSPDMRTPIGHTLAWPKRMETPAESLDFTKLRQMDF
                                                                                                                                                                                                                                                GPFRITSLAEMATVIPERAVQHPNWSMGAKISIDSATMMNKGLELIEAYHLFQIPLEKFE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 999.5; DB 12; Length 388;
Pred. No. 3.2e-89;
4; Mismatches 109; Indels 9;
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RESULT 13

SEQ ID NOS:

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APPLICANT: Gobarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT PILING DATE: 2003-03-28
FRIOR APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCTUS01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOPTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: Sphingomonas trueperi US-10-381-779-97
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isogrepoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
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                                                                                                                                                                                                                                                                            Sequence 103, Application No. US20 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 CLPALQERLAGS----GVEAMGGAHSVCDVARM-GADWTMAAIVGSAGLKPVMAALEAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAAEQLAVLVHRQSVVHSMVEYVDGSVLAQLGTPDMRTPIAYALAWPERMETLCPPLDLA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IILTASGGPFRATPKEAMRDITPAQAVAHPNWSMGAKISVDSATMMNKGLELIEAFHLFP
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D. US20030219798A1
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CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTMARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 121
SEQ ID NO 121
LENGTH: 394
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; TYPE: PRT
; ORGANIAM: Synechocystis sp. PCC 6803
US-10-381-779-103
                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Synechocystis sp. PCC 6803
US-10-381-779-121
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Publication No. US20030219798A1
GENERAL INFORMATION:
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Best Local Similarity 47.3%;
Matches 183; Conservative (
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Best Local '
                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                  Matches
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
FILS REFERENCE: 12904/002US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 VILANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCM---PAGYTPGHTAKQARRI 177
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61 KVAEFKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
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                                                                                                  1 MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPBYAVVVMBS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYDHIDIVIHPQSIIHSLIEVQDTSVLAQLGWPDMRLPLLYALSWPERIYTDWEPLDLVK 293
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                                                 VKRISILGSTGSIGTOTLDIVTHHPDAFQVVGLAAGGNVALLAQQVAEFRPEIVAIRQAE 61
                                                                                                                                                                45.0%; Score 892.5; DB 12; Length 394;
47.3%; Pred. No. 1e-78;
ative 63; Mismatches 128; Indels 13;
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                                                                                                                                                                                                                 Length 394;
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                                                                                                                                                                                                                                                                        121
 354
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                                                                            VGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIE 357
                                                                                                                  TYPHIDIVIHPOSIIHSLIEVOOTSVLAQLGWPDWRLPLLYALSWPERIYTDWEPLDLVK 293
                                                                                                                                                                               VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCM---PAGYTPGHTAKQARRI 177
KTCDLYVGQNTASPDLETTLAADQWAR 380
                                                                                                                                                                                                            LLTASGGPERRIPIETLSSVTPDQAVAHPKWDMGRKISVDSATWANKGLELIEACLLENM 237
                                                                                                                                                                                                                                                                                                     RSMAQFKPDDAGS--LELVLQADQDAR 382
                                                           AGSLSFREPDHDKYPCMQLAYGAGRAGGAMPAVLNAANEQAVALFLQEKISFLDIPRLIE 353
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Search completed: January 29, 2004, 16:21:15 Job time: 27.8953 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004
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364 KPDDAGSLELVLQADQDAREVA 385	306 QRPDEQRFPCLRLASQAAETGGSAPAMLMAANSVAVAAFLERHIRFSDIAVIIEDVLNRE 365	SIMPTVLNAAN:	246 VVIHPQSVIHSMVDYVDGSVIAQLGNPDMRTPISYAMAMPERIDSGVSPLDMFAVGRLDF 305	244 VVIHPQSIIHSMYDTYDGSYLAQWGNPDWRTPIAHAMAWPERFDSGYAPLDIFEYGHMDF 303	186 GPFRETPLEQLASVTPEQACAHPNWSMGRKISVDSASMMNKGLELIEACWLFDAQPSQVE 245	184 GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPDQIE 243	126 ANKEALVMSGALFMQAVKRSGAVILLPIDSEHNAIFQSLPRNYADGLERVGVRRILLTASG 185	124 ANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG 183	67 ALQGSLAAAGIR-TRVLFGEQALCEVASAPEVDMVMAAIVGAAGLPSTLAAVEAGKRVLL 125	-E	7 ISVLGATGSIGLSTLDVVQRHPDRYEAFALTGFSRLAELEALCLRHRPVYAVVPEQAAAI 66	GATGS I GVSTLDVVARHI	y Match 61.2%; Score 1215.5; DB 2; Length 396; Local Similarity 64.1%; Pred. No. 4.9e-84; hes 245; Conservative 48; Mismatches 88; Indels 1; Gaps 1;	rfamily: conserved hypothetical protein HI0807	TIOS:	s-references: GB:AE004785; GB:AE004091; NID:g9949809; PIDN:AAG07038.1; GSPDB:GNOOL: rimental source: strain PAO1	TO>	us: preliminary	ssion: E83188	e: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc rence number: A82950: MITD:20437337: pwID:10984043		; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas,	m, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey,	: 15-Sep-2000 #sequence_revision i5-Sep-2000 #text_change 31-bec-2000 ssion: BB3188		y-d-xylulose 5-phosphate reductoisomerase PA3650 [imported] - Pseudomonas aeruginos

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C;Species: Est
C;Date: 12-Sep
C;Accession:
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64741
A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA
A;Residues: 1-398 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL162752;
A;Experimental source: serogroup
C;Genetics:
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A; Residues: 1-394 < PAR>
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Matches 216
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;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
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      S-AKLLKTMLQQQGSRTEVLSGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKT
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erfamily: conserved hypothetical protein HI0807 words: nucleotide binding; P-loop -119/Region: nucleotide-binding motif A (P-loop
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                                                                                                                                                                                                                                                                        idues: 1-398 <HAY>
ss-references: GB:BA000007; PIDN:BAB33598.1; PID:g13359631; erimental source: strain O157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.; Makino, K.; Ohnishi, M.;
N.; Yasunaga, T.; Kuhara, S.;
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KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLFTLAAAKAGKT 120
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                                                                                     MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES 60
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                                                                                                                                                                                                                  hypothetical protein HI0807
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                                                    Score 1045; D
Pred. No. 3.5e
6; Mismatches
                                                                                                                                                         Pred.
                                                                                                                                                                          Score 1044;
                                                                                                                                   Mismatches 119;
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Shiba, T.; Hattori,
                                                                                                                                                         No. 4.2e-71;
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м.; Shinagawa,
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A;Coss-references: GB:AE005174; NID:g12512898; PIDN:AAG54475.1;
A;Cross-references: GB:AE005174; NID:g12512898; PIDN:AAG54475.1;
A;Cross-references: GB:AE005174; NID:g12512898; PIDN:AAG54475.1;
A;Cross-references: GB:AE005174; NID:g12512898; PIDN:AAG54475.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-200:
C;Accession: G88501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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Best Local
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IERSMAQFKPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                      CKLSALTFAAPDYDRYPCLKLAMEAFEQGQAATTALNAANEITVAAFLAQQIRFTDIAAL
                                                                                                                        NMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAMPERFDSGVAPLDI
                                                                                                                                                                                                                   RILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLF
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                                                                                        FEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVI
                                                                                                                                                                                                SILLTGSGGPERETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLBYIBARWLF
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K.; Apodaca,
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                                                                  09-Nov-2001 #sequence_revision sion: AF0529
1111, J.; Dougan, G.; James, K.D.; Connerton, P.; Cronin, A.; Davi oule, S.; O'Gaora, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; e: Complete genome sequence of Neisseria meningitidis serogroup B rence number: A81000; MUID:20175755; PMID:10710307 ssion: A81229
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                                                                                                                                                          /-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-) es: Salmonella enterica subsp. enterica serovar Typhi this species has also been called Salmonella typhi
   413, 848-852, 2001

rs: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

Complete genome sequence of a multiple drug resistant

ence number: AB0502; MUID:21534947; PMID:11677608
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cimental source: serogroup
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1040.5;
Pred. No. 7.6e
                                                                                        K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Davis, P.; Davies, R.M.; Dowd, L.; White, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                           09-Nov-2001 #text_change
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                    Skelton, J.; Steven Salmonella enterica
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; Dougherty,
; Pizza, M.
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                                  Stevens,
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T-deoxy-D-xylulose 5-phosphate reductoisomerase VC2254 [imported] - Vibrio cholerae (Str C;Species: Vibrio cholerae (C;Species: Vibrio cholerae (C;Species: Vibrio cholerae (C;Species: Naug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: D82099 R;Heidelberg, J.F; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwium, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A,Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: D82099 A;Status: preliminary A,Wolecule type: DNA A;Residues: 1-402 <HEID A;Cross-references: GB:AE004297; GB:AE003852; NID:9955810; PIDN:AAF95398.1; GSPDB:GN001 A;Bxperimental source: serogroup O1; strain N16961; biotype El Tor C;Superfamily: conserved hypothetical protein HI0807 C;Superfamily: conserved hypothetical protein HI0807
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C;Superfamily: conserved hypothetical protein
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 <PAR>
A;Cross-references: GB:AL513382;
C;Genetics:
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                                                                                                        51.5%; Score 1023; llarity 52.7%; Pred. No. 1.60 Conservative 65; Mismatches
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                                                                                                                            ; DB 2;
1.6e-69;
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        I FEVGHMDFEKPDLKRFPCLRLAYEAI KSGGIMPTVLNAANEI AVEAFLNEEVKFTDI AV
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ession: AG0128
khill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre e 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               le: Genome sequence of Yersinia pestis, the causative erence number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cies: Yersinia pestis
e: 02-Nov-2001 #sequence_revision 02-Nov-2001
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                                                                                                                      RRILLTASGGFFRRTPIETLSSVTFDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLL
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                                                                                               SRIILIGSGGPFRETPLSQFSDVTPDQACAHPNWSWGRKISVDSATMMNKGLEYIBARWL
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FNASAEQIEVVLHEQSVIHSMVRYHDGSILAQMGTPDMRTPIAHAMAYPMRVSSGVAPLD
                                    FNMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLD
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55.0%;
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;; Pred. No. 2.7e-69;
51; Mismatches 120;
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GSPDB:GN0012

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1-deoxy-D-xylulose 5-phosphate reductoisomerase XF1048 [imported] - Xylella fastid C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C;Accession: H82728 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

8;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800
                   A,Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
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50.6%;
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6; Mismatches Ill;
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Pred. No. 2.

    Haemophilus influenzae (strain Rd

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2.6e-68;
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Led to GenBank, June 2000

ors: Ferreira, W.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigre M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marrins, E. ors: Martins, B.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. ues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasaki ors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaira cance number: A59328
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T.; Watanabe, A.; Yamada, M.; Ya
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C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: P84957
C;Accession: P84957
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
Nature 407, 81-86, 2000
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A;Experimental source: strain APS
C;Genetics:
A;Gene: dxr; BU235
C;Superfamily: conserved hypothetical protein
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A;Molecule type: DNA
A;Residues: 1-398 <STO>
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: conserved hypothetical protein H10807
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                                                                                                              KVAEFKORIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT
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                                                                                                                                                                                                                                                                                                          conserved hypothetical protein HI0807
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                                                                                                                                                                                                                                     83;
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                                                                                                                                                                                                                                 Score 891; DB 2;
Pred. No. 1.4e-59;
13; Mismatches 127
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es. 8, 205-213, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       etics:
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                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KVAEFKQRIA---ASPVADIKVISGSEALQQVATLENVDTVNAAIVGAAGILPTLAAAKA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIVITGSGGPFYKFSSSDISNVTPDQACSHPNWIMGKKISVDSATMMNKGIBYAEARWIF
                                                     CIELVCDRHQNDNCANPSLDDILAADQWARQEVLTATKNLAS
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                                                                                                                                                          IFEVGHMDFEKPDLKRFPCLRLAYBAIKSGGIMPTVLNAANBIAVBAFLNBEVKFTDIAV 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEVGHMDFEKPDLKRFPCLRLAYBAIKSGGIMPTVLNAANBIAVBAFLNEEVKFTDIAVI
                                                                                                                            LVKAGNLTFREFDHQKYPCMQLAYAAGRAGGSMPAVLNAANEQVVALFLDEKIKFLDIFR
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                                                                                                                                                                                                                                                                                                          RRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLL
                                                                                                                                                                                                                                                                                                                                                 GKDIALANKETLIAGGPVVLPLVEKHGVKLLPADSEHSAIFQCLQGVPKG------GL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VXSITLVGSTGSIGTQTLDIVSQYPDQFRIVGLAAGSNVBMLAEQIRQFRPQIAAISAAE 61
                                                                                    IIERSMAQFKPDDAG--SLELVLQADQDAREVARDIIKTLVA 394
                                                                                                                                                                                                   FGLDYQDIEIVIHPQSIIHSLIELQDTSVLAQLGWPDMRLPLLYALSWPERIYTDWERLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.6%; Score 865; DB 2; ilarity 44.8%; Pred. No. 1.3e-57; Conservative 76; Mismatches 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein HI0807
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                                                         391
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1-deoxy-D-xylulose 5-phosphate reductoisomerase [imported] - Caulobacter crescentus C;Specias: Caulobacter crescentus C;Specias: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: H87486
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeSoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
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C;Superfamilv:
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A;Molecule type: DNA
A;Residues: 1-399 <STO>
A;Cross-references: GB:AE005673; NID:gl3423370; PIDN:AAK23892.1; GSPDB:GN00148
Search completed: January 29, 2004, 15:55:30 Job time : 12.5928 secs
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A;Accession: H87486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPFRRTEIETLSSVTEDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEEDQIE 243
                                                                                                                   |: ::| : | | | :| :::
| NSLGDLSVAESDAVETAMLIDGSARRIAABVV 392
                                                                                                                                                                                                                                                                         EKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVII----ER- 358
                                                                                                                                                                                                                                                                                                                                                                                                             VVIHPQSIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGHMDF 303
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                                                                                                                                                                            -SMAQFKPDDAGSLELVLQADQDAREVARDII 389
                                                                                                                                                                                                                                                                                                                                                           VVIHPOSVIHSLVEYVDGSTLAQLGPPDMRAPIACAFAWPDRLPWPAPRLDLAAYGQLTF 300
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	379	406	379	413	392	418	396	379	475	390	388	380
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ALIGNMENTS	DXR_CHLTR	DXR_MYCLE	DXR_CHLMU	DXR_MYCTU	DXR_CORGL	DXR_STRCO	DXR_DEIRA	DXR CHLPN	DXR MENPI	DXR_FUSIN	DXR BACSU	DXR LISIN
	084074 chlamydia t	Q9cbu3 mycobacteri	Q9pkw8 chlamydia m	Q10798 mycobacteri	Q8np10 corynebacte	Q9kys1 streptomyce	Q9ru84 deinococcus	Q9z8j8 chlamydia p	Q9xes0 mentha pipe	Q8r622 fusobacteri	031753 bacillus su	Q92c37 listeria in

PRINE_RICC 15692 / PAO1; ETRAIN=ANTCC 15692 / PAO1; EXDILINE=20437337; PubMed=10984043; EXPLINE=20437337; PubMed=10984043; ECREY M.J., Brinkman F.S.L., Hufnagle M.O., Kowalik D.J., Lagrou M., A !CREY M.J., Brinkman F.S.L., Hufnagle M.O., Kowalik D.J., Lagrou M., A !CREY M.J., Brinkman F.S.L., Folger K.R., Kas A., Larbig K., Lim R.M., A !CREY M.J., Spencer D.H., Wong G.K.-S., Mu Z., Paulsen I.T., A !Izer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an pportunistic pathogen."; Lure 406:959-964(2000). 1- FUNCTION: Catalyzes the NADP-dependent rearrangement and reduction of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythritol 4-phosphate (MEP). 1- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+) 1- BIZYME REGULATION: INHIBITED BY PGSMIDOMYCIN AND 3-(N-ACETYL-N HYDROXYAMINO)-PROPYLPHOSPHONIC ACID (FR-900098). 9KGU6; 5-OCT-2001 5-OCT-2001 3-FEB-2003 is SWISS-PROT entry is copyright. It is produced through a collaboration stween the Swiss Institute of Bioinformatics and the EMBL outstation - be European Bioinformatics Institute. There are no restrictions on its e by non-profit institutions as long as its content is in no way dified and this statement is not removed. Usage by and for commercial tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch). maa H.; Tools for discovery of inhibitors of the 1-deoxy-D-xylulose -phosphate (DXP) synthase and DXP reductoisomerase: an approach with nzymes from the pathogenic bacterium Pseudomonas aeruginosa."; MS Microbiol Lett. 190:329-333(2000). EQUENCE FROM N.A., AND CHARACTERIZATION. 3DLINB=20487113; PubMed=11034300; 1tincicek B., Hintz M., Sanderbrand S., 5-OCT-2001 (Rel. 40, Created) 5-OCT-2001 (Rel. 40, Last sequence update) 3-PEB-2003 (Rel. 41, Last annotation update) -deoxy-D-xylulose 5-phosphate reductoisomerase -deoxy-D-xylulose 5-phosphate reductoisomerase -ductoisomerase) (1-deoxyxylulose-5-phosphate r seudomonadaceae; DBI_TaxID=287; seudomonas aeruginosa. ucteria; Proteobacteria; ER OR PA3650. SIMILARITY: BELONGS TO THE DXR FAMILY. PSEAE STANDARD; Pseudomonas. Gammaproteobacteria; Wiesner J., A Pseudomonadales; e (EC 1.1.1.267) (DXP reductoisomerase). Beck E.,

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Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415.497-502(2022).
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28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (D)
reductoisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase).
DXR OR RSC1410 OR RS05282.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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FUNCTION: Catalyzes the NADP-dependent reary of 1-deoxy-D-xyluiose-5-phosphate (DXP) to 2 4-phosphate (MEP) (By similarity) CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
DXR OR VV11866.
                                                                                                                                                         Q8DBF5;
15-SEP-2003
15-SEP-2003
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Rhee J.H.,
                                                                       3acteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                      DXR VIBVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_00183; -; :
InterPro; IPR003821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoprene biosynthesis; Oxidoreductase; NADP; VP_BIND 7 14 NADPH (POTENTIAL
               STRAIN=CMCP6
                                                                                                    /ibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGREAMS;
                                                         CBI_TaxID=672;
                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              = 1-deoxy-D-xylulose 5-phosphate + NADPH.
PATHWAY: Nonmevalonate terpenoid biosynthesis
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AMs; TIGR00243; Dxr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL646064; CAD15112.1; -.
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                                                                                                                                                                                                                                                                                                                                                                           HMDEEKDDLKREPCLRLAYBAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERS
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                                                                                                                                                                                                                                                                                                                       MAQEKPDDAGSLELVLQADQDAREVARDII
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 Kim S.Y.,
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                                                                                                                                                                                                                      STANDARD;
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Pred. No. 6.7e-71;
9; Mismatches 109;
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; 5A995A7C8FF32E9D CRC64;
    <u>7</u>.
   J.J.,
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(See http://www.isb-sib.ch/announce/
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Best Local
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Q9JX33;
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"Complete genome sequence Submitted (DEC-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00183; -;
InterPro; IPR003821;
Pfam; PF02670; DXP_re
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                   reductoisomerase) (1-deoxyxylulose-5-phosphate
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                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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NP_BIND 7 14 NADPH (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mplete genome sequence of Vibrio vulnificus CMCP6.";
mitted (DEC-2002) to the EMBL/GenBank/DDS databases.
FUNCTION: Catalyzes the NADP-dependent rearrangement and
of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-
4-phosphate (MEP) (By similarity).
CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate
= 1-deoxy-D-xylulose 5-phosphate + NADPH.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVAEFKORIAASPVA-DIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGK 119
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Pred. No. 8.9e-69;
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irkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
ivee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
ivies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
igels K., Leather S., Moule S., Mungall K., Quail M.A.,
ijandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
intehead S., Spratt B.G., Barrell B.G.,
complete DNA sequence of a serogroup A strain of Neisseria
iningitidis Z2491.";
iture 404:502-506(2000).
iture 404:502-506(2000).
i PULNCTION. Catalyzes the NADP-dependent rearrangement and reduction
of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythritol
4-phosphate (MEP) (By similarity).
i CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
i - PATHMAY: Nonmevalonate terpenoid biosynthesis pathway; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tween the Swiss Institute of Bioinformatics and the EMBL outstation be European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way whited and this statement is not removed. Usage by and for commercial itities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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BDLINE=20222556; PubMed=10761919;
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@RAIN=Z2491 / Ser
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MAP; MF_00183; -; 1.
terPro; IPR003821; DXP_redisomrase
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                                                                                                                                                                PP02670; DXP_reductoiscm; 1.
Ms; TIGR00243; Dxr; 1.
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KPDDAGSLELVLQADQDAREVARDIIKTL
                                                                                                            EKPDLKRFPCLRLAYBAIKSGGIMPTVLNAANBIAVBAFLNEBVKFTDIAVIIBRSMAQF
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Pred. No. 4.1e-68;
9; Mismatches 123;
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Q87ME3;
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Vibrionaceae; Vibrio.
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15-SEP-2003 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF 00183; -; 1.
Isoprene biosynthesis; Oxidoreductase; NADP; (
NP_BIND 7 14 NADPH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are not be the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of the company of
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SIMILARITY: BELONGS
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NTHWAY: Nonmevalonate terpenoid biosynthesis
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                          LEYIEAKWLENAARDQLKVIIHEQSVIHSWVQYRDGSVLAQWGEPDWATDIALTMSYPSR
                                                                      LELIEACLLENMEPDQIEVVIHPOSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPER
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42, Last sequence update)
42, Last sequence update)
42, Last annotation update)
42, Est annotation update)
65-phosphate reductoisomerase (EC 1.1.1.267) (D)
61-deoxyxylulose-5-phosphate reductoisomerase).
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Pred. No. 1e-67
57; Mismatches
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) to 2-C-methyl-D-erythritol
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN=KI2 / W3110;

Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.

Takemoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichiha

Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi

"Systematic sequencing of the Escherichia coli genome: analysis

"Systematic omin (189,987 - 281,416bp) region.";

4.0 - 6.0 min (189,987 - 281,416bp) region.";
                                                                                                                                                                                                                                                                                                                                                                                                                    Blattner F.R., Plunkett G. III, Bloch Riley M., Collado-Vides J., Glasner J.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=98374274; PubMed=9707569;
Takahashi S., Kuzuyama T., Watanabe H., Seto H.;
"A 1-deoxy-D-xylulose 5-phosphate reductoisomerase of cormation of 2-C-methyl-D-crythricol 4-phosphate in nonmevalonate pathway for terpenoid biosynthesis.";
Proc. Natl. Acad. Sci. U.S.A. 95:9879-9884(1998).
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01-NOV-1997
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                                                                                 MEDIINE=93077430; PubMed=1447125; Yamanaka K., Ogura T., Niki H., Hiraga S.; Tamanaka K., Ogura T., Niki H., Hiraga S.; Tidentification and characterization of the of the mukB null mutant of Escherichia coll. J. Bacteriol. 174:7517-7526(1992).
                                                                                                                                                                                            Davis K., Fed
Lashkari D.,
                                                                                                                                                                                                                                                                                                                                                                                              Gregor J., Davis
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15-SSP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
                      Danchin
                                                                                                                                                                       Submitted
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                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   Science
"Detection of new genes in three gene classes.";
                                  Barodovsky M.,
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                                               MEDLINE=96032851;
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K., Federspiel N.
ri D., Lew H., Li
                                                                                                                                                                                                                                                                                                                                                                   nplete genome sequence of 277:1453-1474(1997).
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                                               PubMed=7567469,
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Hyman R., K
D., Namath
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             þ
                                    Koonin
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             bacterial
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                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                   E.V.,
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Kuzuyama T. Takahashi S. Takagi M., Seto H.;

"Characterization of 1-deoxy-D-xylulose 5-phosphate reductoisomerase, an enzyme involved in isopentenyl diphosphate biosynthesis, and identification of its catalytic amino acid residues.";

J. Biol. Chem. 275:19928-19932(2000)

-i- FUNCTION: Catalyzes the NADP-dependent rearrangement and reduction of the catalytic and the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the NADP-dependent rearrangement and reduction of the catalyzes the catalyzes the catalyzes the catalyzes th
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Eisenreich W., Bacher A., Zenk M.H., Arigoni D.;
"Biosyntheeis of terpenoids: 1-deoxy-D-xylulose-5-phosphate
reductoisomerase from Escherichia coli is a class B dehydrogenase.";
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MEDLINE=20123893; PubMed=10631325;
                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrito 4-phosphate (MEP).
4-phosphate (MEP).
CARLYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+) = 1-deoxy-D-xylulose 5-phosphate + NADPH.
COPACTOR: REQUIRES A DIVALENT CATION; MAGNESIUM, MANGANESE OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBÛNIT: Homotetramer.
SIMILARITY: BELONGS TO
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U70214; AAB08602.1; -.
D13334; -; NOT_ANNOTATED
                                                                                                                                                                               al Similarity
219; Conser
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S-AKLLKTMLQQQGSRTEVLSGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKT
                                 KVASFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT
                                                                                                            MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
                                                                                       MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEA
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G-D: DECREASE IN ACTIVITY.

H-Q: INCREASE IN YM.

H-Q: INCREASE IN ACTIVITY.

E-K: DECREASE IN ACTIVITY.

H-Q: INCREASE IN YM.

RTPIAHTM -> VRQLPTPW (IN REF. 3

RTPIAHTM -> VRQLPTPW (IN REF. 3)
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56; Mismatches
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DLINE=21156:31; PubMed=11288796;

Tyashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama in C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T. ihara S., Shiba T., Hattori M., Shinagawa H.;

Jomplete genome sequence of enterohemorrhagic Escherichia coli 157:H7 and genomic comparison with a laboratory strain K-12.":

The Res. 8:11-22(2001).

1- FUNCTION: Catalyana
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757
CR_ECO57
3X8Y1;
3-FEB-2003
8-FEB-2003
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                                                                                                                                                                      FUNCTION: Catalyzes the NADP-dependent rearrangement and reduction of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythritol 4-phosphate (MEP) (By similarity).

1- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+) = 1-deoxy-D-xylulose 5-phosphate + NADPH.

2- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                grma N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., 38e D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Sfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Fotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K. podaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., glch R.A., Blattner F.R.;
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EDLINE=21074935; PubMed=11206551;
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ERAIN=0157:H7 / E
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{Rel. 41, Last sequence update}
{Rel. 41, Last annotation update}
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InterPro; IPR003821; DXP_redisomrase.
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EMBL; AP002550; BAB33598.1; -.
                            MEDLINE=21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
Procent Replace of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

-i. FUNCTION: Catalyzes the NADP-dependent rearrangement and reduction of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-c-methyl-D-erythritol
4-phosphate (MEP) (By similarity).

-i. CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
                                                                                                                                                                                                                                                 SEQUENCE PROM N.A.
STRAIN=Pm70;
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Isoprene biosynthesis; Oxidoreductase; NADP; Complete
NP BIND 7 14 NADPH (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                            Pasteurella multocida.
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              1-deoxy-D-xylulose
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Last annotation update)
(Posphate reductoisomerase (BC 1.1.1.267) (DXP)
(Posphate reductoisomerase).
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Pred. No. 1.
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Fiam, PF02670; DXP reductoisom; 1.
FIGRPAMS; TIGR00243; DXr; 1.
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                                        SEQUENCE FROM N.A.
STRAIN=MC58 / Serogroup B;
MEDLINB=20175755; PubMed=10710307;
                                                                                                                                                                                                                                                             Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro; IPR003821; DXP_redisomrase
PF02670; DXP_reductoisom; 1.
Ms; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    66 RLEALLKRDGTA-TQVLHGAQALVDVASADEVSGVMCAIVGAVGLPSALAAAQKGKTIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESKVA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                              VVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAMPERFDSGVAPLDIFEVGHMDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTVLL 123
                                                                                                                                                                                                                                                                                  GPFRTIPIETLSSVIPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLENMEPDQIE
                                                                                                                                                                                                                                                                                                                                                 ANKETL VVSGALFMETARANGAAVLPVDSEHNAVFQVLPRDYAGRLNEHGIASIILTASG
                                                                                                                                                                                                                                                                                                                                                                                        ANKBALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG
FSDGIGDIGGLEAQDARTRAQARAFIGTL
                                       KPDDAGSLELVLQADQDAREVARDIIKTL 392
                                                                                 QKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAAVAAFLDGQIKFTDIAKTVAHCLAQD
                                                                                                                           EKPELKRFPCLRLAYEAIKSGGIMFTVLNAANEIAVEAFLNEEVKFTDIAVIIERSMAQF
                                                                                                                                                                       VVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAYCLGLPERIDSGVGDLDFDALSALTF
                                                                                                                                                                                                                                                           GPFLTADIATFORITPAQAVKHPNWRMGRKISVDSATMMNKGLELIEAHWLFNCPPDKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .GESTLDVVSRHPEKFRVFALAGHKQVEKLAAQCQTFHPEYAVVADAEHAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41920 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1040.5; D
Pred. No. 3e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA85397E5BE7BD2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rearrangement and reduction to 2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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RESULT 10 DXR_SALTY

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8-FEB-2003 (Rel. 41, Last sequence update)
9-FEB-2003 (Rel. 41, Last annotation update)
-deoxy-D-xylulose 5-phosphate reductoisomerase
-deoxy-D-xylulose 5-phosphate reductoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     his SWISS-PROT entry is copyright. It is produced through a collaboration etween the Swiss Institute of Bioinformatics and the EMBL outstation he EUROpean Bioinformatics Institute. There are no restrictions on its is by non-profit institutions as long as its content is in no way odified and this statement is not removed. Usage by and for commercial intities requires a license agreement (See http://www.isb-sib.ch/announce/z send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           hes
                                                                                                                                                                                                                                                                                                                                                                   soprene biosynthesis; Oxidoreductase; NADP; Complete proteome
;P_BIND 7 14 NADPH (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                             tyGene; SG?????; dxr.
;MAAP; MF 00183; -; 1.
nterPro; TPR003821; DXP redisomrase.
:Eam; PF02670; DXP reductoisom; 1.
IGRFAMs; TIGR00243; DXr; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                almonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XR OR STM0220
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                                                                                                                                                                                                                                                                                                                         y Match
                                                                                                                                                                                                                                                                                                                                                     BOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBL; AE008705; AAL19184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                         local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Catalyzes the NADP-dependent rearrangement and reductio of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrito 4-phosphate (MEP) (By similarity).

CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+) = 1-deoxy-D-xylulose 5-phosphate + NADPH.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE DXR FAMILY.
                   231
                                                180
                                                                                                                                        121
                                                                                                                                                                     19
                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                             VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMP-----AGYTP----GHT
ACLLFNMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGV
                                                                                                                                                                                       KVAEFKQRIAASEVADIKVISGSEALQQVATIENVDTVMAAIVGAAGLLFTLAAAKAGKT 120
                                                S-----ILLIGSGGPFRETPMCDLAAMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIE
                                                                        AKQARRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIE
                                                                                                             ILLANKESLYTCGRLFMDEVKRSNARLLPVDSEHNAIFQSLPQSIQHNLGYADLEQNGVF
                                                                                                                                                                     SAEQLKIMLQQHG-SRTEVLSGQQAACEMAALDEVGHVMAAIVGAAGLLPTLAAIRAGKT
                                                                                                                                                                                                                             MKQLTILGSTGSIGCSTLDVVRHNPDSFRVIALVAGKNVARWAEQCLEFSPRVAVMDDTS
                                                                                                                                                                                                                                                          MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
                                                                                                                                                                                                                                                                                                                                                     398 AA;
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                     43352 MW;
                                                                                                                                                                                                                                                                                                       52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaprotecbacteria;
                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                       Score 1034; DB 1;
Pred. No. 8.8e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                     CB720D959CDF8FCC CRC64;
                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rearrangement and reduction to 2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EC 1.1.1.267) (DXP reductoisomerase).
                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T., Nhan M.,
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hou S., Layman
N., Mulvaney E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Latreille P.,
                                                                                                                                                                                                                                                                                           24;
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                    290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Creitwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
1-deoxy-Discomerase) (1-deoxyxylulose-5-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DXR SAL'
Q8Z9A6;
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 185:2330-2337(2003).

-- FUNCTION: Catalyzes the NADP-dependent rearrangement and reduction of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrito 4-phosphate (MEP) (By similarity).

-- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FKUT 1...
SEQUENCE FKUT 1...
STRAIN=TY2 / ATCC 700931;
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Deng W., Liou S.-R., Plunkett G. C., Blattner F.R.;
RHTland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RHTland V., Kodoyianni V., Schwartz D.C., Blattner Typhi st
                                                      EMBL; AL627266; CAD08678.1; -.
EMBL; AE016834; AA067951.1; -.
HAMAP; MF 00183; -; 1
InterPro; IPR003821; DXP_redis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella
 Pfam; PF02670; DXP reductoisom; 1.
TIGRFAMs; TIGR00243; Dxr; 1.
Isoprene biosynthesis; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of a enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SALTI
                                                                                                                                                                                                                                                                                                  SIMILARITY:
                                                                                                                                                                                                                                                                                                                                   PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355
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                                                                                                                                                                                                                                                                                                                                   1-deoxy-D-xylulose 5-phosphate
NTHWAY: Nonmevalonate terpenoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APLDIFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                  BELONGS TO THE DXR FAMILY
                                                          DXP_redisomrase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reductoisomerase
                                                                                                                                                                                                                                                                                                                      + NAUPH.
biosynthesis pathway; second
                                                                                                                                                                                                                                                                                                                                                         NADPH
       NADP;
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                                                                                                                                                                                                                                                                                                                                                                                                              rearrangement and reduction to 2-C-methyl-D-erythritol
     Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e (EC 1.1.1.267) (reductoisomerase)
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     proteome.
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16-OCT-2001 (Rel. 40, L
28-FEB-2003 (Rel. 41, L
1-deoxy-D-xylulose 5-ph
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16-OCT-2001
16-OCT-2001
28-FEB-2003
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                                                                                                                                                               MEDITINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellet
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J
                                                                                     Nature 406:477-483 (2000)

-i- FUNCTION: Catalyzes the NADP-dependent
-i- FUNCTION: Catalyzes the NADP-dependent
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                                                                                                                                                     Salzberg S.L.,
Fraser C.M.;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=El Tor N16961
                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                      DXR OR VC2254.
Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                           DXR_VIBCH
                                                                                                                             cholerae.
                                                                                                                                       "DNA sequence of
                                                                                                                                                                                                                                                                                              NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                reductoisomerase)
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           SIMILARITY: BELONGS TO THE DXR FAMILY.
                                                            of 1-deoxy-D-xylulose-5-phosphate (DXP) to 4-phosphate (MEP) (By similarity).
CATALYTIC ACTIVITY: 2-C-methyl-D-crythritol
                                      PATHWAY:
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                                                   1-deoxy-D-xylulose 5-phosphate
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41, Last annotation update)
61-phosphate reductoisomerase (EC 1.1.1.267)
61-deoxyxylulose-5-phosphate reductoisomerase
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                                      -phosphate + NADPH.
terpenoid biosynthesis
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49; Mismatches
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                                                  STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
Parkhill J. Wren B.W., Thomson N.R., T
Prentice M.B., Sebaihia M., James K.D.,
                                                                                                                                                                                                                                                                                                                                                                                  Yersinia pestis.
Bacteria; Proteobacteria;
Enterobacteriaceae; Yersin
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
DXR OR YPO1048 OR Y3131.
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HAMAP; MF_00183; -; 1
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          Basham D.,
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52.7%;
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Pred. No. 5.5e-66;
          S.D.,
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          Brooks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
     Titball R.W., Holden M., Churcher C., Mungall ooks K., Cerdeno-Tarraga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nis SWISS-PROT entry is copyright. It is produced through a collaboration stween the Swiss Institute of Bioinformatics and the EMBL outstation for END control on the EMBL outstation for the European Bioinformatics Institute. There are no restrictions on the set by non-profit institutions as long as its content is in no way odified and this statement is not removed. Usage by and for commercial this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parame sequence of Yersinia pestis KIM.";

Bacteriol. 184:4601-4611(2002).

Bacteriol. 184:27es the NADP-dependent rearrangement and of 1-deoxy-D-xylulose-9-phosphate (DXP) to 2-C-methyl-D-4-phosphate (MEP) (By similarity).

- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate 1-deoxy-D-xylulose 5-phosphate + NADPH.

- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; simple statement of the statement
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FRAIN-KIM5 / Biovar Mediaevalis;

FRAIN-KIM5 / Biovar Mediaevalis;

EDLINB-22137863; PubMed=12142430;

EDLINB-22137863; PubMed=12142430;

Erna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.

Etherston J.D., Lindler L.E., Brubaker R.R., Plano

traley S.C., McDonough K.A., Nilles M.L., Matson J.

Erry R.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GRFAMs; TIGR00243; Dxr; 1.
soprene biosynthesis; Oxidoreductase; NADP;
P_BIND 7 14 NADPH (POTENTIAL
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nterPro; IPR003821; I
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FCKVGALTPTTPDYQRYPCLKLAIDACNAGQAATTALNAANEISVMAFLDSKIRPTDIEV
                                                  I FEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMFTVLNAANEIAVBAFLNBEVKFTDIAV
                                                                                                                                       FWMEPDQIEVVIHPQSIIHSMVDTVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLD
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2670; DXP_reductoisom; 1.
TIGR00243; Dxr; 1.
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Pred. No. 8.8e-
51; Mismatches
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D.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gozayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Gogohagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
28-F3B-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (DXP reductoisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P44055;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32763; AAC22466.1; -. PIR; A64014; A64014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DXR_HABIN
                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00183; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Whole-genome random sequencing and
                                                                                                                                                                                                                                                                                                                                        soprene biosynthesis; Oxidoreductase; NADP; Complete proteome PBIND 9 16 NADPH (POTENTIAL).
                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE DXR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                  Pro; IPR003821; DXP redisomrase PF02670; DXP reductoisom; 1.
AMs; TIGR00243; Dxr; 1.
                              62
                                                                                  4.
                                                                                                                                     N
                                                                                                                                                                                                                                 Similarity
VAEFKORIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTV 121
                                                                                     QNIVILGSTGSIGKSTLSVIENNPQKYHAFALVGGKNVEAMFEQCIKFRPHFAALDDVNA
                                                                                                                                        KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003821;
                                                                                                                                                                                                                                                                                                                   397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KW20 / ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                   43667 MW;
                                                                                                                                                                                                                              50.7%;
50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gammaproteobacteria;
                                                                                                                                                                                               Pred. No. 7.5e
6: Mismatches
                                                                                                                                                                                                                              Score 1007; DB 1; Pred. No. 7.5e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                   A6E9B24CC6A1CEAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397
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                                                                                                                                                                                                     111;
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                                                                                                                                                                                                        Indels
                                                                                                                                                                                                  8
                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                        Lee H.J., Kang H.S.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Catalyzes the NADP-dependent rearrangement
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 31821 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION STRAIN-ATCC 31821 / ZM4 / CP4; MEDLINE-20461176; PubMed-11004410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grolle S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reductoisomerase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig. 137-11e S., Bringer-Meyer S., Sahm H.;
"Isolation of the dxr gene of Zymomonas mobilis and characterization of the 1-deoxy-D-xylulose 5-phosphate reductoisomerase.";
FEMS Microbiol. Lett. 191:131-137(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zymomonas mobilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DXIR ZYMMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -deoxy-D-xylulose 5-phosphate reductoisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
                                                                                                                                                                                                                                                                                                                         of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrito 4-phosphate (MEP).
CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                         SUBUNIT: Homodimer.
                                                                                                                                                                                                                                        PATHWAY:
                                                                                                                                                                                                                                                           ENZYME REGULATION: INHIBITED BY FOSMIDOMYCIN.
                                                                                                                                                                                                                                                                                            COFACTOR: REQUIRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
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AJ250714;
AF124757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
                                                                                                                                                                                                                                                                                          1-deoxy-D-xylulose 5-phosphate + NADPH.
OFACTOR: REQUIRES A DIVALENT CATION; MAGNESIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                                                                                        Nonmevalonate terpenoid
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CAB60758.1; -.
AAD29659.1; -.
                                                                                                                                                                                      BELONGS TO THE DXR
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ZM4 / CP4;
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                                                                                                                                                                                          FAMILY.
                                                                                                                                                                                                                                            biosynthesis
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                                                                  oved. Usage by and for (See http://www.isb-sib.
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                                                                                                                                                                                                                                            pathway;
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                                                                                                                        restrictions
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EMBL outstation -
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Search completed: January 29, Job time: 8.41938 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00183; -; 1.
InterPro; IPR003821; DxP redisomrase.
Pfam; PF02670; DxP_reductoisom; 1.
TIGRPAMS; TIGR00243; Dxr; 1.
Isoprene biosynthesis; Oxidoreductase; NADP; Magnesium; Manganese; Cobalt.
Cobalt.
NP_BIND
10 17 NADPH (POTENTIAL).
CONFLICT 226 226 F -> Y (IN REF. 2).
SEQUENCE 388 AA; 41842 MW; 2E161B712089613F CRC64;
                                                                                                                                   124 ANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG 183
||||:||:|:||::||||
123 ANKESLVSAGGLMIDAVREHGTTLLPVDSEHNAIFQCF-----PHHNRDYVRRIIITASG 177
                                                                                                364 KPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                                                                                                                                                                                                                                           178 GPFRTTSLASMATVTPERAVQHENWSMGAKISIDSATMMNKGLELIRAFHLFQIFLEKFE 237
                                                                                                                                                                                                                                                                                               184 GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPDQIE 243
                                                                358 TPATPSSLEDVFAIDNEARIQAAALMESLPA 388
                                                                                                                                                                                                                                                                                                                                                                                                                  67 DLKEALAGS---SVEARAGADALVEARMY-GADWTMAAIIGCAGLKATLAAIRKGKTVAL 122
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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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1985
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Gapop 10.0 , Gapext 0.5
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sp_maumal:*
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sp_vertebrate:*
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SUMMARIES

No.	Score 1062	Query Match 53.5	Query Match Length 53.5 402	16	ID Q8DBF5
N	1041.5	52.5	396	16	Q8EGG9
ω	983	49.5	382	16	Q8KG43
44,	870	43.8	413	16	Q8DKG 0
Ų٦	838.5	42.2	472	10	Q9SP64
σ	827.5	41.7	473	10	Q8L6C5
7	818.5	41.2	397	16	Q8D2G6
6 0	816.5	41.1	475	10	Q947C3
9	810.5	40.8	473	10	Q8W250
10	807.5	40.7	473	10	ONTH 60
11	803.5	40.5	474	10	Q9M4W4
12	802.5	40.4	472	10	Q9FXZ7
13	735.5	37.1	391	16	082146
14	729.5	36.8	488	ທ	096693
15	729.5	36.8	488	ഗ	Q8IKG4
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119 RILLANKEALVMSGQLFIDEVEKSGAQLLEVDSEHNALFQCLPQ-TVQGNLGRCDLASQG 177	120 TVLLANKEALYMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQ 173	59 KEAALRIKWALAVLAPNTQVLGGQEALCYVATLEQVDSVMAAIVGAAGLVPTMAAVKAGK 118	VLSGSBALQQVATLENVDTVMAAIVGAAGI	1 MOKUTILGATGSIGASTLKVIEQNPDKFSVVALAADSNVEKMQQLCQRWQPEYAVMAN 58	PDKYQVVALTANG	23	53.5%; Score 1062	EQUENCE 402 AA; 43352 MW; 13095814BF685BAF CRC64;	6803; AAO:	Thmitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.	;	nee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	RAIN=CMCP6:	SOUTENCE FROM N.A.	UBI_TaxID=672;		acteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	ibrio vulnificus.	-deoxy-D-xylulose 5-phosphate reductoisomerase.	(TrEMBLrel. 23, Last	1_MAR2003 (frequentet. 65, creates)		3DBFS PRELIMINARY; PRT; 402 AA.	1
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01-MAR-2003
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Alteromonadaceae; Shewanella
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NMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERPDSGVAPLDI
                                                                          RILLTASGGPFRRTPIBTLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLF
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                                                 HILLIGSGGPFLTAELSNLAAMTPAQACKHPNWSMGPKISVDSATMMNKGLEFIEARWLF
                                                                                                                                                 VILANKEALVMSGQIFMQAVSDSGAVILPIDSEHNAIFQCMPAGYTPG-----HTAKQAR 175
                                                                                                                                                                                     AALALKAQLPAA--LNIQVTSGEDELIALVTAPAVDTVMAAIVGAAGLVPTLAAVKAGKR
                                                                                                                                                                                                      KVAEFKORIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
                                                                                                                                                                                                                                                     MONMVILGATGSIGASTLSVISANSTAYRVYALVANASVDKMLTLCLAHREQVAHMVDHK 60
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                                                                                                                   VILANKEAL VMSGELFIEATRASGATILE VDSEKNAIFQCLPEEVQSNLGRCDLAASGIS
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
plulose 5-phosphate reductoisomerase.
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                                                                                                                                                                                                                                                                                                                                   52.5%; Score 1041.5; DB 16; Length 396; 55.1%; Pred. No. 2.3e-69;
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C STRAIN=TLS / ATCC 49652 / DSM 12025;

X MEDLINE=22103685; PubMed=12093901;

X MEDLINE=22103685; PubMed=12093901;

X MEDLINE=22103685; PubMed=12093901;

X MEDLINE=22103685; PubMed=12093901;

X MEDLINE=22103685; PubMed=1.T., Heidelberg J.F., Wu M.,

A Deboy R. J., Paulsen I.T., Nelson W.C., Haft D.H.,

A Dodson R.J., Peterson J.D., Durkin A.S., Kolomay J.L., Yang F.,

A Hickey B.K., Peterson J.D., Durkin M.S., Kalomay J.L., Yang F.,

A Hickey B.K., Peterson J.D., Durkin M.S., Kalome D.,

A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

A Venter J.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

Venter J.C., Fettelin H., White O., Gruber T.M., Ketchum K.A.,

Venter J.C., Tettelin H., Bryant D.A., Praser C.M.;

The complete genome sequence of Chlorobium tepidum TIS, a

"The complete genome sequence of Chlorobium tepidum TIS, a

"The complete genome sequence of Chlorobium tepidum TIS, a

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Pfam; PF02670; DXP_reductoisom; 1.
TIGREAMs; TIGR00243; Dxr; 1.
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01-MAR-2003
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11-OCT-2002 (TREMBLrel. 22, Last sequence update)
11-MAR-2003 (TREMBLrel. 23, Last annotation update)
11-MAR-2003 (TREMBLrel. 23, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase.
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                                GHMDFEKPDIKRFPCIRIAYBAIKSGGIMPTVLNAANEIAVBAPLNBBVKFTDIAVIIER
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ATLTÉEEPOMERÉPALRLAFDALKAGQTYPAVLNAANETAVAAFLDKKIGETDTAGTVDK
                                                                                                                                                                                                 LTASGGPERRTPIETLSSYTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNME
                                                                                                                                                                                                                                                                      KTVLLANKBALIMSGQIFMQAVSDSGAVLLPIDSBHNAIFQCMPAGYTPGHTAKQARRIL
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                                                                             PDQIEVVIHPOSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAMPERFDSGVAPLDIFEV
                                                                                                                                                                                                                                          KDIALANKETLVVAGQLVSDLVKKHDVKLLPVDSEHSAIFQSL-----VGHRTEDIERII
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                                                                                                                                                                                                                                                                                                                                                                                                      MKSLSILGSTGSIGLSTLDVVRRHPERFSIAALAEGHDVEMLLKQIDBFRPSLVSVRDEA
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                                                                                                                                                            FKVGQLSFCEPDFNRFPCLALAIEACSQGQEATTVLNAANEIAVEAFLQGKIGFTHIGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 AA; 41343 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 983; DB 1
Pred. No. 5e-65;
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Q9SP64; PRELIMINARY;
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01-JUN-2002 (TrEMBLrel. 2
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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01.MAR-2003 (TrEMBLrel. 23, Last sequence update)
01.MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase.
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L; AP005372; BAC08593.1; -.
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45.4%; Pred. No. 1.5e-56;
tive 76; Mismatches 123;
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rtemisia annua (Sweet wormwood).
.karyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
permatophyta; Magnoliophyta; eudicotyledons; core eudicots;
steridae; campamulids; Asterales; Asteraceae; Asteroideae;
nthemideae; Artemisia.
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3L6C5;
1-0CT-2002
1-0CT-2002
1-MAR-2003
                                                                                                                                      evia rebaudiana (Stevia).

karyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

permatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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bbe K.K., Souret F.F., Shore K.A., Weathers P.
\text{\text{tremisia annua 1-deoxy-D-xylulose-5-phosphate}}
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dBL; AF182287; AAD56391.2; -.
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Pred. No. 3.9e-54;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Wigglesworthia.
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Pfam; PF02670; DXP reductoisom; 1.
TIGRFAMs; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                 flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24534.1; -.
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Aksoy S.;
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EMBL; AJ429233; CAD22156.1;
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Pred. No. 9.4e-
81; Mismatches
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Pred. No. 2.6e-53;
1; Mismatches 129;
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MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANG-NIDALYEQCLAHHPEYAVVVME 59

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MEDLINB=21425086; PubMed=11532167;

MEDLINB=21425086; PubMed=11532167;

Rodriguez-Concepcion M., Ahumada I., Diez-Juez B., Sauret-Gueto
Rodriguez-Concepcion M., Ahumada I., Diez-Juez B., Sauret-Gueto
Lois L.M., Gallego F., Carretero-Paulet L., Campos N., Boronat i
"1-Deoxy-D-xylulose 5-phosphate reductoisomerase and plastid
isoprenoid biosynthesis during tomato fruit ripening.";
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ZMBL, AF331705, AAK96063.2; ---
EnterPro; IDFR003821; DXP_redisomrase.

Pfam; PF02670; DXP_reductoisom; 1.

TIGRPAMs; TIGR00243; Dxr; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
1-deoxy-D-xylulose-5-phosphate reductoisomerase.
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                                                                                                                                                               VAEFKQRIAASPVADI----KVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFTDIAIINKKVLDKLDIFEPSSIEEILLLDSKARNLAKKFIK 395
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GKDIALANKETLIAGGPFVLPPAHKHKVKILPADSEHSAIFQCIQGLPEG-
                                                        GKTVLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQC---MPAGYTPGHTAKQA
                                                                                                                   VESTROAL----ADMEDRATIPGEQGVIEVARHADAVIVVTGIVGCAGLKATVAAIEA
                                                                                                                                                                                                                                 KPISIVGSTGSIGTQTLDIVAENPDKFRVVALAAGSNVTLLADQVKTFRPKLVAVRNESL
                                                                                                                                                                                                                                                                      KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPBYAVVVMESK 61
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Pred. No. 1.7e-52;
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TRANSIT 1 49 POTENTIAL.
SEQUENCE 473 AA; 51497 WW; 618C4A675283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
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Q1-MAR-2002.(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003821; DXP redisomrase.
Pfam; PF02670; DXP reductoisom; 1.
TIGRPAMS; TIGR00243; DXr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carretero-Paulet L., Boronat A., Campos N.;
"1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR),
first committed step of the mevalonate-independent path
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8W250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EC 1.1
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DIFEVGHYDFEKEPLKREPCLRLAYEAIKSGGIMETVLAVAANEIAVEAFLNESVKETDIA
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                                                                                                                MEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPER-FDSGVA--PL
                                                                                                                                                                                      ILLTASGGPFRRTFIETLSSYTPDQAVAHPKWDMGRKISVDSATWMWKGLBLIEACLLFN 236
                                                                                                                                                                                                                                                                                             DIALANKETLIAGGPFVLPLAQKHKVKILPADSEHSAIFQCIQGLPEG-----ALRR
                                                                                                                                                                                                                                                                                                                               TVLLANKEALVMSGQIFMQAVSDSGAVLLPIDSBHNAIFQC---MPAGYTPGHTAKQARR 176
                                                                                                                                                                                                                                                                                                                                                                                               VDELKEALAD----CDWKPEIIPGEQGVIEVARHPDAVTVVTGIVGCAGLKPTVAAIEAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPISIVGSTGSIGTQTLDIVAENPDKFRVVALAAGSNVTLLADQVKTFKPKHVAVENESL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYBQCLAHHPEYAVVVMESK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.8%; Score 810.5; DB J
45.4%; Pred. No. 4.8e-52;
cive 67; Mismatches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
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1-MAR-2001 (TEMBLrel. 16, Created)
1-MAR-2001 (TEMBLrel. 16, Last sequence update)
1-OCT-2002 (TEMBLrel. 22, Last annotation updat-deoxy-d-xylulose-5-phosphate reductoisomerase.
0005A05.19 OR P0482C06.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAIN=cv. Nipponbare; asaki T., Matsumoto T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asaki T., Matsumoto T.,
Oryza sativa nipponbare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         karyota; Viridiplantae; Stre
permatophyta; Magnoliophyta;
prhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ramene; Q9FTNO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ibmitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
dBL; AP002863; BAB16915.1; -.
dBL; AP002845; BAB78606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               one: P0482C06."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR003821; DXP_redisomrase
PF02670; DXP_reductoisom; 1.
AMs; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
DLCKLGSLTFKAPDNVKYPSMDLÄYAAGRAGGTMTGVLSAANEKAVELFIDEKIGYLDIF
                                          DIFEVGHMDFEKPOLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIA 353
                                                                                     ARYDDIEIVIHPOSIIHSMIETQDSSVLAQLGWPDMRIPILYTMSWPDRIYCSEVTWPRL
                                                                                                                 MEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPER-FDSGVA--PL
                                                                                                                                                                        ILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFN 236
                                                                                                                                                                                                                                                                DIALANKETLIAGGPFVLPLAQKHKVKILPADSEHSAIFQCIQGLPEG------ALRR
                                                                                                                                                                                                                                                                                                          TVLLANKBALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQC---MPAGYTPGHTAKQARR 176
                                                                                                                                                                                                                                                                                                                                                       VDELKEALAD----CDWKPEIIPGEQGVIEVARHPDAVTVVTGIVGCAGLKPTVAAIEAGK
                                                                                                                                                                                                                                                                                                                                                                                             VAEFKQRIAASPVADIK--VLSGSEALQQVATLENVDTVMAAIVGAAGLLETLAAAKAGK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                               KPISIVGSTGSIGTQTLDIVAENPDKFRVVALAAGSNVTLLADQVKTFKFKLVAVRNBSL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nipponbare;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.7%; Score 807.5; DB 45.4%; Pred. No. 8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51473 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ databases
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(GA3) genomic DNA, chromosome 1,
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yta; Liliopsida; Poales; Poaceae;
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--RSMAQFKPDDAGSLELVLQADQDAREVARDI 388

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RESULT 12
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AC Q9FXZ
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Best Local S
Matches 176
        Q9FXZ7;
01-MAR-2001
01-MAR-2001
01-JUN-2002
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EMBL; AF250235; AAF63154.1; -.
InterPro; IPR003821; DXP redisomrase.
Pfam; PF02670; DXP reductoisom; 1.
FIGRFAMs; TIGR00243; DXT; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicottyledons; core eudicotts;

Asteridae; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 1.6e-51;
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01-MAR-2003
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"Regulation of the non-mevalonate methylerythritol phosp
pathway by mycorrhizal fungi.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ297566; CAC03581.1;

InterPro; IPR003821; DXP_redisomrase.

Pfam; PF02670; DXP_redisomrase.

Pfam; PF02670; DXP_redisomrase.

IIGRFAMS; TIGR00243; DXr; 1.
                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC DXR OR LA3292.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                Submitted (MAR-2002) to the EMBL/GenBank/DDBJ EMBL; AB011490; AAN50490.1; -.
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                                                                                                        SEQUENCE FROM
STRAIN=56601
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01-MAY-1999
01-MAY-1999
01-JUN-2002
                                                                                                                                                                                                                                                                                                                     Altincicek B., Sanderbrand S., Wiesner J., Jomaa H.;
"dxr as a potential target for antimalarial drugs.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF111813; AAD03739.1; -...
Interpro; IPR003921; Dxr. redisomrase.
Pfam; PF003670; DXP reductoisom; 1.
TIGRPAMS; TIGR00243; Dxr; 1.
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Eukaryota; Alveolata;
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  GKTVLLANKEALVMSGQIFMQAVS-DSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQ---
                                                                                                                  VAIFGSTGSIGINALNII-RECNKIENVFNYKALYVNKSVNELYEQAREFLPEYLCIHDK 138
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                                                                             SKVAEFKORIAASPVADIK--VLSGSBALOOVATLENVDTVMAAIVGAAGLLFTLAAAKA
                                                                                                                                                         ICILGATGSIGVSTLDVVARHPDK----YQVVALTANGNIDALYBQCLAHHPBYAVVVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPDDAGSLELVLQADQDAREVARDI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPDFKRYPGLGLAFEAGKVGGTAFCIFNAANEAAVELFLKDEIRFIEIPDYIRETLDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVIHPQSIAHGIVELKDGASFLYASYPDMIFPIAHSLFHPEPVPKVLRSYPAKDWGKLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAFRELPVEQLSSVTKEQALHHPTWNWGPKITIDSNGMLNKGLEVIEAHFLFNVPYDKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPDQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANKETLVTSGPLIQSLIAKHNTKVVPVDSEHNALFQLLES-LNPNSVEK----IILTASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCLLGASGSVGESTLKVLRAHPEKFRLHSFSVHSNLEKAKEIQKEFSPDF--ICVSSDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391
                                                                                                                                                                                                                                                                                    488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
ylulose 5-phosphate reductoisomerase.
                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                    55756 MW; 4E280C81CDFAD3EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43026 MM;
                                                                                                                                                                                                36.8%; Score 729.5; DB 5; Length 37.8%; Pred. No. 5.4e-46; tive 88; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.1%; Score 735.5; DB 16; Length 41.0%; Pred. No. 1.4e-46; ive 78; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
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ridner M.J., Hall N., Fung B., White O., Berriman M., Hyman R.W., rilton J.M., Pain A., Nelson K.B., Bowman S., Paulsen I.T., James K. sen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., an M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., artea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., ritin D.M.A., Fairlamb A.H., Fraumholz M.J., Roos D.S., Ralph S.A., Fadden G.I., Cummings L.M., Subramanian G.M., Mungall C., nter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., asser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDLINE=22255705; PubMed=12368864;
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Lasmodium falciparum (isolate 3D7)
Ekaryota; Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BL; AE014826; AAN37254.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deoxy-D-xylulose 5-phosphate reductoisomerase.
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-MAR-2003 (TrEMBLrel. 23, Last sequence update)
-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             4 ICILGATGSIGVSTLDVVARHPDK----YQVVALTANGNIDALYEQCLAHHPEYAVVVMB
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                     NKIVALANKESIVSAGFFLKKLINIHKNAKIIPVDSBHSAIFQCLDNNKVLKTKCLQDNF
                                                                                                                                                      GKTVLLANKEALVMSGQIFMQAVS-DSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQ----
                                                                                                                                                                                                          SVYEELKELV--KNIKDYKPIILCGDEGMKEICSSNSIDKIVIGIDSFQGLYSTMYAIMN
                                                                                                                                                                                                                                                        SKVAEFKQRIAASPVADIK--VLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKA 117
                                                                                                                                                                                                                                                                                                               VAIFGSTGSIGTNALNII-RECNKIENVFNVKALYVNKSVNELYEQAREFLPEYLCIHDK
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                                        --ARRILITASGGPFRRTPIETLSSVTPDQAVAHPKWDWGRKISVDSATWMNKGLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55756 MW;
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37.8%; Pred. No. 5.4
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                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 141;
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Job t	В	Ş	改	Ş	ДЪ
Job time : 31.3684 secs	437 YFDISSIISQVLESENSQKVSENSEDLMKQILQIHSWAKDKATDI 481	349 FTDIAVIIERSMAQFKPDDAGSLELVLQADQDAREVARDI 388	377 NLKPLDLAQVSTLTFHKPSLEHPPCIKLAYQAGIKGNPYPTVLNASNEIANNLFLNNKIK 436	289 GVAPLDIPEVGHMDEEKPDLKREPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVK 348	

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; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-309-026-2
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Search completed: January 29, 2004, 15:57:04
Job time: 8.2499 secs
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APPLICANT: Mooney, Jeffrey L.
APPLICANT: Debouck, Christine M.
APPLICANT: Zhong, Yi Yi
TITLE OF INVENTION: No. 6204042el GlmU
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.4%; Score 88.5; DB 3; Length 459; Best Local Similarity 23.9%; Pred. No. 0.12; Matches 48; Conservative 32; Mismatches 74; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GN10024
TELECOMMUNICATION INFORMATION:
TELECHOONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 19103
ZOMPUTER READABLE FORM:
MEDIUM TYPB: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/309,026
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/971,782
PRIOR APPLICATION NUMBER: 08/971,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-994-2222
                                                                                             148 EVLRMVEQKDATDFEKQIKEI 168
                                                                                                                                          177 DALORTEGNPAVTDEASALEL 197
                                                                                                                                                                                                                     125 DTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQM---FKYGML-----R 176
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                                                                                                                                                                                                                                                                                                                                     68 SIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDA---ARPCLTGSDIHLQI 124
                                                                                                                                                                                                                                                                                         47 -----KTVTVVGHK--ASIVEEVLAGQTEFVTQSEQLGTGHAVMMTEPILEGISGHTLV 98
                                                                                                                                                                                                                                                                                                                                                                                    8 WAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPEL 67
                                                                                                                                                                                      ----IAGDTPLITGESLKNL----IDPHINHKNVATILTAETDNPFGYGRIVRNDNA 147
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

5: /cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

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US-09-934-868-68
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Sequence 68, Appl
Sequence 10, Appl
Sequence 11931, A
Sequence 11075, A
Sequence 11722, A
Sequence 10723, A
Sequence 11, Appl
Sequence 13867, A
Sequence 8, Appli
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Sequence 14505, A		Sequence 11824, A	455	Sequence 23443, A	136	823	Sequence 528, App	e 215	264, Ap	10400,	•	Ġ	487,	Sequence 245, App	17444	ø	18528,	Φ		ce 2163	6	Sequence 12467, A				Sequence 13256, A	Φ	Sequence 5711, Ap	Sequence 12471, A

ALIGNMENTS

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Seq. snce 6, Application US/09934903
Pat: It No. US20020102690A1
GEN: JAL INFORMATION:
AP. JICANT: Koffas, Mattheos
AP. JICANT: Odom, J. Martin
AP. JICANT: Schenzle, Andreas J.
AP. JICANT: No. US20020102690Alton, K.
AP. JICANT: Tomb, Jean-Francois
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Best Local Similarity
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JICANT: Cheng, Qiong

LE OF INVENTION: Genes Involved in Isoprenoid Compounds Production

REPERENCE: CL1646 US NA

RENT FILING DATE: 2001-08-22

RAPPLICATION NUMBER: 60/229,907

R FILING DATE: September 1, 2001

JR FILING DATE: September 1, 2001
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DPYWPBLSIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDI 120
                                                      MNPTIQCWAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE
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                                                                                                                                                                   Conservative
                                                                                                                                                          100.0%; Score 1199; DB 10; 100.0%; Pred. No. 2.1e-115; vative 0; Mismatches 0;
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APPLICANT: KOEfas, Mattheos
APPLICANT: Koom, James M

APPLICANT: Ocom, James M

APPLICANT: Schenzle, Andreas J

TITLE OF INVENTION: DENITIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: CL1596 US NA

FILE REFERENCE: C
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PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
SEQ ID NO 68
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09941947A Publication No. US20030003528A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. User:
Patent No. User:
Patent INFORMATION:
Toffas,
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                                                                                                                                                                                                                                                                                                             APPLICANT: Brzostowicz, Patricia C. APPLICANT: Cheng, Qiong APPLICANT: DiCosimo, Deana J.
                                  APPLICANT: Picataggio, Steve
APPLICANT: Rouviere, Pierre E.
TITLE OF INVERTION: CARCYENOID PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REFERENCE: CL1903 US NA
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ORGANISM: Methylomonas
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MNPTIQCWAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTEGNPAVTDEASALELLGHKPKIVEGREDNIKITRPEDLALAQFYMEQQA 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLQIDTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPYWPELSIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
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                                                                                                                                                                                         Odom, J. Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1199; DB 10; ilarity 100.0%; Pred. No. 2.1e-115; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                               Edward S. Jr
US/09/941,947A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 231;
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C TRENT FILING DATE: 2001-09-01
FIOR APPLICATION NUMBER: 60/229,907
FIOR APPLICATION NUMBER: 60/229,858
FIOR APPLICATION NUMBER: 60/229,858
FIOR APPLICATION NUMBER: 60/229,858
FIOR FILING DATE: 2000-09-01
NUMBER OF ESQ ID NOS: 60
S.FTWARE: Microsoft Office 97
SEN ID NO 10
SENGTH: 231
TYPE: PRT
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                                                                                                                                                                           C RENT APPLICATION NUMBER: US/09/815,242
C RENT ETLING DATE: 2001-03-21
ELIOR APPLICATION NUMBER: 60/191,078
ELIOR FILLING DATE: 2000-03-21
ELIOR APPLICATION NUMBER: 60/206,848
ELIOR FILLING DATE: 2000-05-23
ELIOR APPLICATION NUMBER: 60/207,727
ELIOR APPLICATION NUMBER: 60/207,727
ELIOR APPLICATION NUMBER: 60/207,727
ELIOR APPLICATION NUMBER: 60/242,578
ELIOR APPLICATION NUMBER: 60/242,578
ELIOR APPLICATION NUMBER: 60/253,625
ELIOR APPLICATION NUMBER: 60/257,931
ELIOR APPLICATION NUMBER: 60/269,308
ELIOR APPLICATION NUMBER: 60/269,308
ELIOR APPLICATION NUMBER: 60/269,308
ELIOR APPLICATION NUMBER: 60/269,308
ELIOR APPLICATION NUMBER: 60/269,308
ELIOR APPLICATION NUMBER: 60/269,308
ELIOR APPLICATION NUMBER: 60/269,308
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A PLICANT: Trawick, John E
A PLICANT: Carr, Grant J.
A PLICANT: Yamamoto, Rober
E PLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Be t Local 9
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E PLICANT: Ohlsen, Kari L
E PLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: Identification of Essential Genes
TLE OF INVENTION: Prokaryotes
LE REFERENCE: BLITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :uence 11931, Application US/09815242
ent No. US20020061569A1
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                                                                                                                                   FIWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZRAL INFORMATION
RGANISM: Pseudomonas aeruginosa
:-815-242-11931
                                                                                                                                                             MBER OF SEQ ID NOS:
                                                                                ENGTH: 234
                                                                                                      ID NO 11931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DPYWPELSIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNPTIQCWAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 100.0%; Score 1199; DB 11; Similarity 100.0%; Pred. No. 2.1e-115; 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
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Yamamoto, Robert T.
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTMARE: PASTSEQ for Windows Version 4.
SEQ ID NO 11076
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT APPLICATION NUMBER: 60/191.078

PRIOR APPLICATION NUMBER: 60/191.078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/242,578

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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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US-09-815-242-11076
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Best Local
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                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Haemophilus influenzae
                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 GVAITDEASAMEWAGYAPKLVEGRADNLKITTPEDLLRLQ 229
  67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCAASRHVQRAAGGAERAGSVLNGLLRLLELGAQADDWVLVHDAARPNLTRGDLDRLLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIAKHPDIITAPGGKERADSVLSA-LKALEDIASENDWVLVHDAARPCLTGSDIHLQIDT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLIRLLESDAPQKVAVAISVEDPYWPEL 67
L--DPKIQLVEGGTTRAESVLNGLNA---TAEKNAWVLVHDAARPCLQ----HADIDKLL 117
                    IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTVIPAAGVGSRMRADRPKQYLDLAGRTVIERTLDCFLEHPMLRGLVVCLAEDDPYWPGL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAEDPVGGLLAVPARDTLKRSDRDGRVSETIDRSVVWLAYTPOMFRLGALHRALADALVA 189
                                                                          AVLPAAGVGSRMQADKPKQYLTLIGKTLLEHTLDVMLSYPAVSKIILAVSKDDPYISTLS
                                                                                                            AVVPAAGVGKRMQADRPXQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPBLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind, Judith W. Wall, Daniel
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                                                                                                                                                    Conservative
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                                                                                                                                                44.2%; Score 530.5; DB 9;
52.5%; Pred. No. 1.9e-46;
tive 28; Mismatches 65;
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Pred. No. 5.3e-49;
26; Mismatches 72;
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CU RENT FILING DATE: 2001-03-21
CU RENT FILING DATE: 2001-03-21
ER OR RILING DATE: 2000-03-21
PR OR RELICATION NUMBER: 60/206,848
PR OR FILING DATE: 2000-05-23
PR OR REPLICATION NUMBER: 60/207,727
PR OR RILING DATE: 2000-05-26
PR OR PILING DATE: 2000-05-26
PR OR PILING DATE: 2000-10-3
PR OR RELICATION NUMBER: 60/242,578
PR OR RELICATION NUMBER: 60/242,578
PR OR RELICATION NUMBER: 60/253,625
PR OR REPLICATION NUMBER: 60/257,931
PR OR REPLICATION NUMBER: 60/257,931
PR OR REPLICATION NUMBER: 60/257,931
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    815-242-10273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ence 11722, Application US/09815242 at No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAL INFORMATION
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Zyskind, Judith W.
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LICANT: Xu, H. Howard

LE OF INVENTION: Identification of Essential Genes
LE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
SER OF SEQ ID NOS: 14110
TWARE: FASTSEQ for Windows Version 4.0
ID NO 11722
MGTH: 254
                                                                                                                                                                                                                                                                                                                                                                          / Match 44.2%; Score 529.5; DB 9;
Local Similarity 51.1%; Pred. No. 2.9e-46;
les 114; Conservative 30; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 NDPVGGILALSSHDTLKHVD-GDT-ITATIDRKHVWRALTPQMFKYGWLRDALQR--TEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 AIEDKQGAILAIPVTDTIKRADNQQCIVKTEDRSQLWQAWTPQFFPVDILRDALSTGIQQ 177
                                                                                                                                                                                                                                   69 IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCUTGSDIHLQIDTLK 128
LAQHPQITVVDGGAERADSVLAGLQAL----PEAQWVLVHDAARPCLHQDDLSRLLSICE 148
                                                                                                                                                                                                                                                                                                                            AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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                                                                                                 TSRVGGILAAPVRDTMKRAEPGKTAIAHTVDRNDLWHALTPQLFPRELLVDCLTRALNEG
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US-09-815-242-10273
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     APPLICANT: Fritz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: USE OF YACM AND YOEJ, ES
TITLE OF INVENTION: AND THEIR USE
FILE REFERENCE: 06286-140001
CURRENT APPLICATION NUMBER: US/09/792,251
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                      RESULT 8
US-09-792-251-11
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
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Best Local Simi
Matches 111;
                                                                                                                                                                                                                GENERAL INFORMATION:
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Patent No. US20020160364A1
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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NUMBER OF
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L INFORMATION:
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No. US200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AVVPAAGVGKRMQADRÞKQYLÞLAGKTVIEHTLTRLLESDAFQKVAVAISVEDÞYWÞBLS 68
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Zyskind, Judith W.
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Trawick, John D.
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Yamamoto, Robert T.
                                                                                                                                                                                                                                                              Application US/09792251
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                                                                                                                       ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
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US-()-815-242-13867
                                                                                                                                                                                                                                                                                                                                                                                    ICE REFERENCE: ELITRA.011A
CREENT PILING DATE: 2001-03-21
LIOR APPLICATION NUMBER: 60/191,078
LIOR APPLICATION NUMBER: 60/191,078
LIOR APPLICATION NUMBER: 60/206,848
LIOR APPLICATION NUMBER: 60/207,727
LIOR APPLICATION NUMBER: 60/207,727
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LIOR APPLICATION NUMBER: 60/242,578
LIOR APPLICATION NUMBER: 60/253,625
LIOR APPLICATION NUMBER: 60/253,625
LIOR APPLICATION NUMBER: 60/257,931
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)RGANISM: Escherichia coli
)-792-251-11
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PLICANT: VI, H. Howard

TLE OF INVENTION: Identification of Essential Genes

TLE OF INVENTION: Prokaryotes
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ID NO 13867
ENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                   IMBER OF SEQ ID NOS: 14110
                                                                                        THER INFORMATION:
                                                                                                              OCATION: (1)...(
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ry Match
                                                       -815-242-13867
                                                                                                                                                                                                                                       YPE: PRT
                                                                                                                                                                                                                RGANISM: Salmonella
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                                                                                                                        (236)
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                                                                                           Xaa = Any Amino Acid
   Score 499.5;
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   DB 9;
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   Length 236
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RESULT 11
US-09-935-943-8
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US-09-792-251-8
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                                                                                                 Sequence B, Application US/0935943
Patent No. US20020120963A1
GENERAL INFORMATION:
APPLICANT: Levin, Joshua Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09792251
Patent No. US20020160364A1
GENERAL INFORMATION:
APPLICANT: Wegrich, Lynette M.
APPLICANT: Budziszewski, Gregory J.
TITLE OF INVENTION: Herbicide Target Genes
FILE REFERENCE: pB/5-31509A
CURRENT APPLICATION NUMBER: US/09/935,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fritz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Daz-Maria
TITLE Guzman, Luz-Maria
TITLE OF INVENTION: USE OF YACM AND YOEJ, SSSENTIAL BACTERIAL GENES AND POLYPEPTIDES
TITLE OF INVENTION: AND THEIR USE
FILE REFERENCE: 06286-140001
CURRENT APPLICATION NUMBER: US/09/792,251
CURRENT FILING DATE: 2001-02-23
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                  ERKGFLGTDDASLVEQMEGGSVRVVEGSYTNÍKLTTPDDLTSAEAIMESES 227
                                                                                                                                                                                                                                                                                                         EGNPAV-TDEASALELL-GHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
                                                                                                                                                                                                                                                                                                                                                   ELIAEAEQTGAAILAVPVKDTIKRVQDLQVSETIERSSLWAVQTPQAFRLSLLWKAHAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ATITDEASALEYCGFHPALVEGRADNIKVTRPEDLALAEFYL 227
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                                           and Methods
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Bes: Local :
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SAL INFORMATION:

LIAPTING PROMOTION:

LIAPTING PROMOTION:

LIAPTING PROMOTION:

Genes Involved in Isoprenoid Compound Production

E REFERENCE: CL-1788

ERNT APPLICATION UNUMBER: US/10/128,713A

UENT FILING DATE: 2002-04-22

UENT FILING DATE: 2002-04-22
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73: PRT
AANISM: Rhodococcus erythropolis
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OR APPLICATION NUMBER: PCT/EP01/08910
OR FILING DATE: 2001-08-01
OR APPLICATION NUMBER: US 60/222,779
OR FILING DATE: 2000-08-03
BER OF SEQ ID NOS: 26
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174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 IFEEYEESIDVDLRFAIPGKERQDSVYSGLQEI-DVNSE--LVCIHDSARPLVNTEDVE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VVPAAGVGKRMQADRPKQYLPLAGKTVIEH---TLTRLLESDAFQKVAVAISVEDPY---
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                                                                                                QIDTLKNDPVGGILALSSHDTLKHVDG-DTITATIDRKHVWRALTPQWFKYGMLRDALQR 181
                                                                                                                                                         -----SIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHL 122
                                                                                                                                                                                                                                     AVVPAAGVGKRMQADRPKQYLPLAGKTVIBHTLTRLLESDAFQKVAVAISVEDPYWPEL-
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-AGDVAATDDAALVERLGVSVQTIPGDALAFKITTPLDLVLAR
                               TEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQ 224
                                                                 VVDALRAGSSAVIPVLPVTDTIKSVDVLGAVTGTPLRSELRAVQTPQGFSTDVLRSAYD-
                                                                                                                                   ESVVADLGRASDVDVVGGGAERTDSVRAGLSA----AGDADFVLVHDAARALTPPALIAR 114
                                                                                                                                                                                                      ALVPAAGRGVRLGEKLPKAFVELGGCTMLARAVDGLRKSGAIDRVVVVIVP-----PELV 58
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                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                      21.3%; Score 255.5; DB 1 35.0%; Pred. No. 4.8e-18; tive 30; Mismatches 96
                                                                                                                                                                                                                                                                                                         DB 12;
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; ORGANISM: Chlamydia pneumoniae US-10-289-762-621
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US-10-156-761-11503
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US-10-156-761-11503
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
TSHIKAWA, JUN
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 621
LENGTH: 218
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 621, Application US/10:
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffais, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11503
LENGTH: 250
                                                                                   Matches
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                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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APPLICANT: HORIGAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                            Local Similarity
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                                                                              74;
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3 PTIQCWAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAJSVEDP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAI-----SV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFDRDTLVRAHETVTDNVTDDASMVEQLGARVVVVPGHEBAFKVTRPLDLVLAE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMLRDALQRIEGNPA--VIDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDAVIEAVRDGAPAVVPALPLADTVKQVEPAAVPGEPEPVVATPERARLRAVQTPQ----
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                                                                                 Conservative
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                                                                              20.1%; Score 240.5; DB 12; Length 218; 32.9%; Pred. No. 1.5e-16; tive 41; Mismatches 91; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 250;
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR ETLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6422
LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6422, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOFIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
190
                                          178 ALOR -- TEGNEAV -- TDEASALELIGHKEKIVEGREDNIKITREEDLALAO 224
                                                                                       130 IARVVRKVHEGATAVÍPVLÞVSDTIKRVSPDGGVVVDTPNRAELRAVQTÞQGFLLSELVA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 LAKEKOLTLVDDIRAABIIGKPSQLVFNKHPQIKISYPEDLTIAQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 QIDTLKNDPVGGILALSS--HDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDALQ 180
                                                                                                                                                                               70
                                                                                                                                                                                                                68 ----SIAKHPD----IITAPGGKERADSVLSALKALE-DIASENDWVLVHDAARPCLTGSD 119
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                                                                                                                                                                          LRKRGLLNDPEGVRVRLVHGGGERADSVWAGLQAISLDDATPDAIVLIHDSARALTPPGM 129
                                                                                                                                                                                                                                                                  ALLAAAGRGTRLGGPIPKAFVTLRERTLLERSLQAMLTSESVDBIIILVSPDMETYARDL 69
                                                                                                                                                                                                                                                                                                             AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE-DPYWPEL 67
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ANEKFFADPNPGFIPTDDASLMEWYGADVVCVQGDPMAFKVTTPIDMMLAQ 240
                                                                                                                                IHLQIDTLKNDPVGGILALSSHDTLKHV--DGDTITATIDRKHVWRALTPQMFKYGMLRD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RTEGNPAVTDEASALELLGHKPKIVEGRPONIKITRPEDLALAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DLLETAEKIGATALASPIPYTIKORNP---VRTLDRDNLAIIHTPOCIKTEILREGLA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PMIKSSLILLSGGQGTRFGSKIPKQYLPLNGTPLVLHSL-KILSS--LPQIAEVIVVCDP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YOKOI, HARUHIKO
TATBISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANDO
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                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                       1B.6%; Score 223.5; DB 10; Length 256; 30.7%; Pred. No. 1.1e-14; tive 43; Mismatches 102; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 256;
                                                                                                                                                                                                                                                                                                                                                          Gaps
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Search completed: January 29, 2004, 16:21:16 Job cime : 16.7685 secs

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OM protein - protein search, using sw model
                                                                                                                      Title:
Perfect score:
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    Searched:
                                                              Scoring table:
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                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                 US-09-941-947A-10
1199
1 MNPTIQCWAVVPAAGYGKRM.....IKITRPEDLALAQFYMEQQA 231
                                                                                                                                                                          January 29, 2004, 15:44:49; Search time 6.79678 Seconds {without alignments} 3268.453 Million cell updates/sec
283308 seqs, 96168682 residues
                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters:

283308

Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	₽B	ID	Description
1	4.	- 1	232	2	C82311	2-C-methyl-D-eryth
Ŋ	555.5	46.3	234	N	F83191	served hypothe
w	0	4.	225	N	G64156	cal prot
4		ü	236	N	A91079	l prot
ហ	4.	<i>ن</i> ب	236	N	B85924	l prot
σ .	.0		236	N	G65055	4-diphosphocytidyl
7	'n	ω	236	Ŋ	AE0856	2-C-methyl-D-eryth
8	Ņ	Ņ	241	Ŋ	AC0408	4-diphosphocytidyl
9	4.	œ	237	Ŋ	F84978	hypothetical prote
10	٠,	٠.	229	N	D81867	conserved hypothet
11	·	4.	229	N	H81073	
12	378		231	N	H82700	
13	٠	φ	228	2	C83663	O
14	Θ	7	232	Ŋ	-	3
15	ထ	·	213	Ŋ	\mathbf{r}	conserved hypothet
16	282.5	23.6	228	N	AG2451	-diphosphocytidy
17		'n	400	Ŋ	w	ispd/ispf bifuncti
18	279.5	ū	400	Ŋ	U1	5
19	272	ν.	474	N	S60902	CDP-ribitol pyroph
20	270	'n	232	N	0	2-C-methyl-D-eryth
21	268.5	2	222	N	B72259	র্ন্থ
22		:	232	N	σ	2-C-methyl-D-eryth
23	260.5		230	N	S76158	<u>~</u>
24	254.5	۲	231	N	0	_
25	254.5	1.	241	N	A86949	al I
26	246	0.	236	N	,	Ö
27		0	390	N	AI3359	Ď
28	234.5	9	211	N	H72061	ė
29		19.6	211	N	H86562	2-C-methyl-D-eryth
						-

RESULT 2
P83191
Conserved hypothetical protein PA3633 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Oate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 17-Mar-2003
C;Acccuston: P83191
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri

4. U:	4.0	4 3	43	.4 .	40	ω te	ω ©	ω ~2	(ည () ()	ري U1	S S	υ Ω	U U	ω. L.	30
118	131.5	141	146.5	170.5	190.5	200.5	201.5	209	209	211	214.5	225	227	227	233.5
9.8	11.0	11.8	12.2	14.2	15.9	16.7	16.8	17.4	17.4	17.6	17.9	18.8	18.9	18.9	19.5
458	371	229	189	278	399	238	218	235	235	232	238	382	379	237	229
Ŋ	2	N	N	N	N	2	N	N	N	N	N	Ŋ	N	N	N
C86860	E81256	B71148	B71511	T00613	G71314	F89788	C81669	F95147	D9801S	D75254	389789	F87464	S34980	AF1566	F97291
hypothetical prote	hypothetical prote	hypothetical prote	2-C-methyl-D-eryth	2-C-methyl-D-eryth	conserved hypothet	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	conserved hypothet	conserved hypothet	conserved hypothet	hypothetical prote	2-C-methyl-D-eryth	4-diphosphocytidyl

ALIGNMENTS

D 97	B &	B &	₽ Q	Query Ma Best Loo Matches	A;Gene: VC0528 A;Map position C;Superfamily: C;Keywords: nu	A;Status: p A;Molecule A;Residues: A;Cross-ref A;Experimen C;Genetics:	A;Title A;Refer A;Acces	R;Heide chardso	C#2311 2-C-methyl C#Species: C#Accession
182 TEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQ 229	127 LKNDPVGGILALSSHDTLKHVDG-DTITATIDRKHVWRALTPQMFKVGMLRDALOR 181 -	69 IAKHPDIITAPGGKERADSVLSALKALEDIASENDWYLVHDAARPCLTGSDIHLQIDT 126	9 AVVPAAGYGKR%QADRP%QYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS 68 	Query Match 47.9%; Score 574.5; DB 2; Length 232; Best Local Similarity 54.4%; Pred. No. 4.5e-41; Matches 124; Conservative 28; Mismatches 63; Indels 13; Gaps 5;	A;Gene: VC0528 A;Map position: 1 C;Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol synthase C;Key√ords: nucleotidyltransferase	A;Otatus: preliminary A;Molecule type: DNA A;Redicus: 1-232 <hei> A;Residus: 1-232 <hei> A;Cross-references: GB:AE004139; GB:AE003852; NID:g9654953; PIDN:AAP93696.1; GSPDB:GN001; A;Experimental source: serogroup O1; strain N16961; biotype El Tox C:Genetics:</hei></hei>	A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: C82311	R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. Chardson, Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.	CR321L 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (BC 2.7.7.60) - Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Mar-2003 C:Accession: CR311

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Mar-2003
C;Accession: G64156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein HI0672 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
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Nature 406, 959-954, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01,
A;Reference number: A32950; MUID:20437337; PMID:10984043
A;Accession: F83191
A;Status: preliminary
                                                                                                                                                                                     , D
                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:U32750; GB:L42023; NID:g1573668; PIDN:AAC22332.1; PI
A;Note: best homolog was a hypothetical protein from Rhodobacter capsulatus
C;Superfamily: 4-diphosphocytidy1-2-methy1-D-erythritol synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:AE004783; GB:AE004091; NID:g9949786; PIDN:AAG07021.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid s
A;Molecule type: DNA
A;Residues: 1-225 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. Reference number: A64000; MUID:95350630; PMID:7542800
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-234 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: G64156
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                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 117
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Best Local S
Matches 119
                                                                                                                                                                                                                                                                                                                   Local Similarity
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                   AIEDKQGAILAIPVTDTIKRADNQQCIVKTEDRSQLWQAMTPQFFPVDILKDALSTGIQQ 177
                                                                                                               L--DPKIQLVEGGTTRAESVLNGLNA---IAEKNAWVLVHDAARPCLQ----HADIDKLL
                                                                                                                                       IAMEPDIITAPGGXERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DCAASRHVQRAAGGAERAGSVLNGLLRLLELGAQADDWVLVHDAARPNLTRGDLDRLLEE
                                                              --NDPVGGILALSSHDTLKHVDG-DTITATIDRKHVWRALTPQMFKYGMLRDALQR-TEG 184
                                                                                                                                                                                                      AVLPAAGVGSRMQADKPKQYLTLLGKTLLEHTLDVMLSYPAVSKIILAVSKDDPYISTLS
                                                                                                                                                                                                                                                 AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTVIPAAGVGSRMRADRPKQYLDLAGRTVIERTLDCFLEHPMLRGLVVCLAEDDPYWPGL
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                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                44.2%; Score 530.5; DB 2; 52.5%; Pred. No. 2.2e-37;
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Best Local S
Macches 112
                                                                                                                                  ;Gene: ygbP
;Superfamily:
                                             Macches
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  AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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#;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
A;Tirle: Computer ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypochetical protein ygbP [imported] - Escherichia coli (strain 0157H7, substrain C;Sp.coles: Escherichia coli (strain 0157H7, substrain C;Sp.cole: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-Mar-2003 C;Accession: B85924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-236 <HAY>
A;Residues: 1-236 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37024.1; PID:g13363072; GSPDB:GN00154
A;Cross-references: GB:BA000007; PIDN:BAB37024.1; PID:g13363072; GSPDB:GN00154
A;Reperimental source: strain O157:H7, substrain RIMD 0509952
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C;Accession: A91079

R;Hayashi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; F
gasewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: A91079
                                                                                                                                                                                                       A;Cross-references: GB:AB005174; NID:g12517201; PIDN:AAG57854.1; GSPDB:GN00145; UWGP:Z40
A;Experimental source: strain O157:H7, substrain EDL933
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C;Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol synthase
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A; Residues: 1-236 <STO>
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A;Reference number: A85480; MUID:21074935; PMID:11206551
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                                Similarity
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                                                                                                                       4-diphosphocytidyl-2-methyl-D-erythritol synthase
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50.2%;
                                43.7%; Score 524.5; DB 2
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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, K.M.; S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;fittle: Complete genome sequence of a multiple drug resistant A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0856
A;Status: preliminary
                                                                                                                           2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [imported] - Salmon (7,Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-Mar-2003 C;Accession: AE0856 C;Accession: AE0858 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, V. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, S.; Moule, S.; O'Gaora, P.
                                                                                                                                                                                                                                                                                                     RESULT 7
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A.; Rose, D.J.; Mau, B.; Shao,
Science 277, 1453-1462, 1997
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;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
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49.8%; Pred. No. 1.7e-36;
tive 31; Mismatches 72;
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Y.
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                                                                             Skelton, J.; Stevens
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, L.; White,
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A;Molecule type: DNA
A;Residues: 1-236 <PAR>
'A;Cross-references: GB:J
C;Genetics:
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A;Status: preiss.
A;Molegule type: DNA
A;Molegule type: LAI < KUR>
- manidues: 1-241 < KUR>
- manidues: GB:AL590842;
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-diphosphocytidyl-2C-methyl-D-erythritol synthase C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 C;Accession: AC0408
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C;Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol
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Best Local :
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.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-Mar-2003
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                          NPAVTDEASALELIGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQ 230
                                                                                        NDFVGGILALSSHDTLKHVDG--DTITATIDRKHVWRALTPQMFKYGMLRDALQRT--EG
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                                                                   CSQVGGILAAPVRDTMKRAEPGIQAIAHTVDRQDLWHALTPQLFPLELLKLCLSRALREG
                                                                                                                                           VAQDPRISTVYGGDQRANSVMAGIQ----LAGQAEWVLVHDAARPCLHLDDLSRLLSITE
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                                                                                                                                                                                                                                                                                                    Score 512.5; DB Pred. No. 8e-36;
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Pred. No. 4.4
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hypothetical protein [imported]
C;Species: Buchhera sp.
C;Date: 02-Mar-2001 #sequence_re
C;Accession: F84978
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A;Title: Genome sequence of the endocellular bacterial symbiont
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: F84978
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A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81867
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein NMA1713 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 17-Mar-2003
C;Accession: D81867
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajand Nature 404, 502-506, 2000
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A;Experimental source: strain AP
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A; Residues: 1-237 < STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISVTDEASALEYCGYNPLLVLGSCRNIKITWPEDLVLANFYLK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NDPVGGILALSSHDTLKH--VDGDTITATIDRKHVWRALTPOMFKYGMLRDALCR-TEGN 185
                                              TAFPQVRVWKN
                                                                                     --WPELSIAKHPDIITAPGGKERADSVLSAL-KALB-DIASENDWVLVHDAARPCLTGSD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAVIDEASALELIGHKPKIVEGRPONIKITRPEDLALAQFYME 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNPVGAILARPVSDTIKYSNLKQKKAVYTVYRKNLWHALTPQLFQVELLKNCLKKIIKDQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVVPAAGVGKRMQADREKQYLELAGKTVIEHTLTRLLESDAFQKVAVAISVEDEYWEELS
  IHLQIDTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDAE 179
                                                                                                                                                                          AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISSNFRIISVVGGEKRINSVLSGLIVVKNV----DWVIVHDAVRPCLSYKDLEKLISIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAKHPDIITAPGGKERADSVISALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIVPAAGIGSRMKIDVPKQYIKIQNRTILEHTLTTLLHPNIVQIIVSLNKKDNYFHKLS
                                                                                                                              ALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDTFADKVQ
                                                                                                                                                                                                                                                                                                      4-diphosphocytidyl-2-methyl-D-erythritol synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4-diphosphocytidyl-2-methyl-D-erythritol synthase
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                        34.3%;
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    Buchnera sp.

                                                                                                                                                                                                                     48
                                           GGOTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEA 119
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Pred. No. 1.
                                                                                                                                                                                                                                        Score 411.5; DB:
Pred. No. 2.5e-27
                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67;
                                                                                                                                                                                                                                                             Length 229;
                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 237;
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Rajandream
                                                                                                                                                                                                                                                                                                                                                                                           PID:9738035
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H81073
                A;Experimental source: strain 9a5c
R;Skipson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, Briories, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Caraso, B.; Docena, C.; Bl_Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                               A;Ti:le: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      日
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                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
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                                                                                                       A;Residues: 1-231 <SIM>
A;Crss-references: GB:AE003962; GB:AE003849; NID:g9106270; PIDN:AAF84102.1; GSPDB:GN001
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GenBank,

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A;Cross-references: GB:AE002501; GB:AE002098; NID:g7226755; A;Experimental source: serogroup B, strain MC58 C;Genetics:
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Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein NMB1513 [imported] - C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #
C;Accession: H82700
R;anonymous, The Xylella fastidiosa
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: NMB1513
C; Superfamily:
                                                                                          C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Mar-2003
                                                                                                                                                    conserved hypothetical protein XF1293 [imported] - Xylella fastidiosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-229 <TET>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 TAFFQVRVWYO------GGQTRÁETÝRNGVAKLLETGLAAETDNILVHDÁÁRCCLPSEA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 --WPELSIAKHPDIITAPGGKERADSVLSAL-KALE-DIASENDWVLVHDAARPCLIGSD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90;
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                                                                                                                                                                                                                                                                                                                                 QRTEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYME 228
                                                                                                                                                                                                                                                                                                                                                                                                               LTRLIEQAGNAAEGGILAIPIADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVVDAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IHLQIDTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDAL
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                                                                                                                                                                                                                                                                                                  -AAENLDGITDEASAVEKLGVRPLLIQGDVRNLKLTQPQDAYIVRLLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDTFADKVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.2%;
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Pred. No. 3.7e-27;
9; Mismatches 73
                                       Consortium of the Organization for
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                                             Nucleotide Sequen
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strain MC58.
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A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu chado, M.A.; Madeira, A.M.B.N.; Wadeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Wathors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa., R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A;Duthors: da Silva, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, R.G.; Gallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Q. R. Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-228 <STO>
A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03826.1; GSPDB:GN00
A;Experimental source: strain C-125
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83663
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                                                                                                                                                                                                                                                                                                                                                       DTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDALQRTEG 184
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Pred. No. 1.7e-24;
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A;Cross-references: EMBL:D26185; NID:g467326; PIDN:BAA05324.1; PID:g467478
A;Note: the nucleotide sequence was submitted to the EMBL Data library, December 1993
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Elrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Odega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zunstein, E.; Yoshikawa, H.; Danchin, A. A;Accession: R69580; MUID:98044033; PMID:9384377
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #text_change 17-Mar-2003
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2003
C;Accession: D70414
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grah
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                                                                                                                                              conserved hypothetical protein ad 1323 - Aquifex aeolicus
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A; Residues: 1-232 < KUN>
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A; Residues: 1-232 < OGA>
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ce: strain 168
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-213 <AQF>
A;Cross-references: GB:AE000734; NID:g2983733; PIDN:AAC07307.1; PID:g2983746; GB:AE00065
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: aq 1323
C;Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol synthase
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300, MUID:98196666; PMID:9537320
A;Accession: D70414
Search completed: January 29, 2004, 15:55:30 Job time: 6.79678 secs
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AVVPAAGVGKEMQADRPKQ AVVPAAGVGSEMKADRPKQ	ilarity Conserva	116802; AAO1 -00108; -; 1PR001228; 11128; ISD3; TIGR00453; PS01295; IS PS01295; IS PS01295; AA; 237 AA;		enome sequence DEC-2002) to th N: Catalyzes th D-erythritol fr te (By similari IC ACTIVITY: CT hate + 4-(cytid Nonmevalonate TY: BELONGS TO	OM N.A. 6; Kim S.Y.	33 (Rel. 42, Created) 33 (Rel. 42, Last sequence u 53 (Rel. 42, Last sequence u 53 (Rel. 42, Last sequence u 54 (Rel. 42, Last sequence u 55 (Rel. 42, Last sequence u 56 (Rel. 42, Last sequence u 57 (Rel. 42, Last sequence u 58 (RCT) 59 (Rel. 42, Last sequence u 59 (Rel. 42, L	STAN		11111111111111111111111111111111111111
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15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF 00108; -; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP005081; BAC60822.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Ta
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC (4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP cytidylyltransferase) (MCT).
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                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Catalyzes the formation of 4-diphosphocytidy1-2c-methy1-D-erythritol from CTP and 2C-methy1-D-erythritol 4-phosphate (By similarity).

CATALYTIC ACTIVITY: CTP + 2-C-methy1-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methy1-D-erythritol.

FATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third ste SIMILARITY: BELONGS TO THE ISPD FAMILY.
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European Bioinformatics Institute. There are no restrictions on
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                                                         IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                                  AIVPAAGVGSRMKADRPKQYLLIDGKTVLEHTVEKLLAHPQIAKVVVAVTEGDPYYPELS
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IALHPDVIRVAGGKERADSVLSGLNYV-SAQLPCEWVLVHDAARPCVTLNDIDRLIDVCC 128
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Pred. No. 7.9e
30; Mismatches
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Matches
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Best Local :
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PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis; Complete proteome.
SEQUENCE 232 AA; 25901 Mar.
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2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (BC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
cytidylyltransferase) (MCT).
ISPD OR VCDSS8
                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a clear the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
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STRAIN-EI TOR N16961 / Serotype 01;

MEDLIXE-20406833, PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Pleischmann R.D., Nierman M.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
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InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; ISPD 1.
PIRSF; PIRSF006765; DPCME synth; 1.
                                                                                                                                                                                                          PIR; C82311, C82311.
HSSP; Q46893; 1152.
TIGR; VC0528; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae.
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                                                                                                                                                                                                                                                                                           send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-PHOSPHATE BY SIMILARITY).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphosphat)-2-C-methyl-D-erythritol.
PATHWAY: Nonmevalonate tergenoid biosynthesis pathway; third stepsingly: BELONGS TO THE ISPD FAMILY.
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                                                                                                                                                                                                                                                          AE004139; AAF93696.1; -.
                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHPTGGILASPVRDTMKRANKENNIDHTVDREALWHALTPQMFKTQQLTRALADALQQ--
                                                                                                                                                                                                                                                                                                        requires a license agreement
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio.
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                 47.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gammaproteobacteria; Vibrionales;
28;
             Score 574.5; DB 1
Pred. No. 4.4e-43;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232
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                              DB 1;
   Indels
                              Length
                                                                                                                                                                                                                                                                                                                                                       restrictions
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnaghe W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino B., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.B.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.", Mature 406:959-964(2000).

Nature 406:959-964(2000).

Nature 406:959-964(2000).

NATURE ORDERSTRIBUTED FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-METHYL-D-ERYTHRITOL FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-
                           TIGREAMS; TIGRO0453; ispD; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                   HAMAH, MF 00108; ; 1.
InterPro; IPR001228; ISPD synthase.
Pfam; PF01128; IspD; 1.
PIRSF; PIRSF006765; DPCME_synth; 1.
                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by arentities requires alicense agreement (See http://www.isborsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 15692
MEDLINE=20437337;
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16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cyridylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
                                                                    rigrfams;
                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHATE (BY SIMILARITY).

CATALITIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third step.

SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                               F83191; F83191.
; Q46893; 1152.
                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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 25613 MW;
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2CBA037CD85B42C9 CRC64;
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                                                                                                                                                                                                                                                                                                               There are no restrictions
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1 S., Yuan Y.,
K., Lim R.M.,
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Best Local :
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institution. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMeder7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kærlavage A.R., Bult C.J., Tomb J.-F., Dougherry B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1SPD HAI
005029;
               HSSP; Q46893; 1152.
TIGR; H10672; -.
                                                    EMBL; U32750; AAC22332.1; PIR; G64156; G64156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae
Eacteria; Proteobacteria; Gan
Easteurellaceae; Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C1-NOV-1997 (Rel. 35, Last sequence update)
29-FBB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythricol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol - PATHWAY: Normevalomate terpenoid biosynthesis pathway; third strict SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: CATALYZES
D-ERYTHRITOL FROM CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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54.1%;
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CTP AND 2C-METHYL-D-ERYTHRITOL 4-PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gammaproteobacteria; Pasteurellales;
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Haar C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Yabe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:17 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

-I- FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-2C-methyl-Derythritol 4-phosphate.

-I- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

-I- COFACTOR: Magnesium, manganese or cobalt (By similarity).
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PIRSF; PIRSF006765; DPCME synth;
TIGRFAMs; TIGR00453; 1spD; 1.
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KEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
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Q8X7\(\frac{7}{4}\)
Q8-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylltransferase
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP)
Cytidylyltransferase) (MCT) (CDP-ME synthetase).
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=0157:H7 / R
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Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
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Best Local &
SEQUENCE FROM N.A.

STRAIN=06:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plumkett G. III, Redford P., Ro
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N
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of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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[15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythricol 4-phosphate cytidylyltransferase
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
cytidylyltransferase) (MCT).
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InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; ISpD; 1.
PIRSP; PIRSP006765; DPCM3_synth; 1.
TIGRPAMs; TIGR00453; ispD; 1.
                                                                                                                                                                                                                                                                                            Enterobacteriaceae,
NCBI_TaxID=217992;
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PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                      Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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INIT_MET 0 0 BY SIMILARITY
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B85924; B85924.
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BAB37024.1; -.
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No. 1e-38;
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SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERI STRAIN-K12 / DH5-alpha; STRAIN-K12 / DH5-alpha; MEDLINE=99449755; PubMed=10518523; Rohdich F., Wungsintaweekul J., Fellermeier M., Sagr Kis K., Bisenreich W., Bacher A., Zenk M.H.; "Cytidine 5'-triphosphate-dependent biosynthesis of protein of Escherichia coll catalyzes the formation diphosphocytidyl-2-C-methylerythritol.";
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'InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; ISPD; 1.
TIGRFAMS; TIGR00453; ispD; 1.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
(4-diphosphocytidyl-2-methyl-D-erythritol synthase) (MEI
cytidylyltransferase) (MCT) (CDP-ME synthetase).
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CATALYTIC ACTIVITY: CTP +
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32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21320925; PubMed=11427897;

Hilho A.M., Cane D.E., Noel J.P.;

hillo A.M., Cane D.E., Noel J.P.;

Structure of 4-diphosphocytidyl-2-C-methylerythritol synthetase
involved in mevalonate-independent isoprenoid biosynthesis.";

Mat. Struct. Biol. 8:641-648(2001).

Mat. Struct. Biol. 8:641-648(2001).

Mat. Struct. Biol. 8:647-648(2001).

MAT. STRUCTION: CARALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-

D-ERYTHRITOL FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-PHOSPHATE.

MAT. STRUCTLY ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate =

diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

MANGANESE OR COBALT.

COPACTOR: MAGNESIUM, MANGANESE OR COBALT.

COPACTOR: Nonmevalonate terpenoid biosynthesis pathway; third step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Cregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I Mau B., Shao Y.;
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STRAIN-KL2 / W3110;

Kuzuyama T., Takagi M., Kaneda K., Dairi
"Formation of 4-(cytidine 5'-diphospho)-
2-C-methyl-D-crythritol 4-phosphate by 2
4-phosphate cytidylyltransferase, a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: OPTIMAL PH IS 8.3. SIMILARITY: BELONGS TO THE ISPD FAMILY.
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ne 5'-diphospho)-2-C-methyl-D-erythritol from
. 4-phosphate by 2-C-methyl-D-erythritol
. 14-phosphate by 2-C-methyl-D-erythritol
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K., Mayhew G.F
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP cytidylyltransferase) (MCT).
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 MBDLINE=21534947; PubMed=11677608; Parkhiil J., Dougan G., James K.D., Thomson N. Churcher C., Mungall K.L., Bentley S.D., Holde Baker S., Basham D., Brooks K., Chillingworth
                                                                   STRAIN-CT18
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               ISPD SALTI
Q82471;
                                                                                                                NCBI_TaxID=601;
                                                                                                                                Enterobacteriaceae;
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                                                                                                                                                                  Salmonella typhi
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Thomson N.R., Pickard
S.D., Holden M.T.G., Se
llingworth T., Connerto
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SEQUENCE
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MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                                                                                                                                                                                                                                                                                                                  EMBL; ABO16843; AAO70388.1; -.
HAMAP, MF 00108; -; 1.
InterPro; IPR001228; ISPD_synthase.
Pfam; PP01128; IspD; 1.
PIRSF; PIRSF006765; DPCME synth; 1.
TIGR00453; ispD; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
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between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 185:2330-2337(2003).

PINCTION: Catalyzes the formation of 4-diphosphocytidyl-2C-methyl-D-crythritol from CTP and 2C-methyl-D-crythritol 4-phosphate (By similarity).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-crythritol 4-phosphate = CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-crythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-crythritol.

PATHWAY: Nonmevalomate terpenoid biosynthesis pathway; third step-similarity: BELONGS TO THE ISPD FAMILY.
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                                                                                     NDPVGGILALSSHDTLKHVD--GDTITATIDRKHVWRALTPQMFKYGMLRDALQR--TEG
                                                                                                                                   LÄNHPQITVVDGGNERADSVLAGLQAV----AKAQWVLVHDAARPCLHQDDLARLLAISE
                                                                                                                                                                                                                                                                                                                                                  proteome.
                                NPAVTDEASALELIGHKPKIVEGRPDNIKITRPEDLALAQFYM
                                                                                                                                                                                                AVVPAAGFGRRMOTECPKOYLSIGNKTILEHSVHALLAHPRVTRVVIAISPGDHRFAQLP
-ATITDEASALEYCGFHPALVEGRADNIKVTRPEDLALAEFYL
                                                                                                                                                   AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
                                                                 nsrvggilaspvrdtmkrgepgkna i ahtveradi whaltpoppprelihdci tralneg
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                                                                                                                                                                                                                                                                  43.0%; Score 515.5; DB 1;
49.8%; Pred. No. 6.4e-38;
49.8%; Mismatches 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 236 AA;
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TIGRFAMS; TIGR00453; ispD; 1.
PROSITE; PS01295; ISPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00108; -; 1.
InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; IspD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioliformatics and the EMEL outstation the European Bioliformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Salmonella.
 Q8ZB<u>P</u>6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP cytidylyltransferase) (MCT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphate (By similarity).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third step SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-2C-methyl-D-erythritol from CTP and 2C-methyl-D-erythritol 4-
                YERPE
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                                                                                                                             NPAVTDEASALELIGHKPKIVEGRPDNIKITRPEDLALAQFYM
                                                                                                                                                                     NSRVGGILASPVRDTMKRGEPGKNAIAHTVERADLWHALTPQFFPRELLYDCLTRALNEG
                                                                                                                                                                                                                                       LANHPOITVVDGGNERADSVLAGLQAV----AKAQWVLVHDAARPCLHQDDLARLLAISE 125
                                                                                                                                                                                                                                                                        IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                                                                                                                                                                                                                           AVVPAAGFGRRWOTECPKOYLSIGNKTILEHSVHALLAHPRVTRVVIAISPGDHRFAQLP 69
                                                                                                                                                                                                                                                                                                                                    AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAPQKVAVAISVEDPYWPELS 68
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                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                25755 MW;
                                                                                                                                                                                                                                                                                                                                                                                             42.8%;
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                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                            ; Score 513.5;
; Pred. No. 9.6e
32; Mismatches
                PRT;
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                24 I
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thes 71;
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                                                                                                                                   227
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S., Layman D.,
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MEDINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Bakker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quall M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                           EMBL; AJ414156; CAC92591.1; -.
EMBL; AE013685; AAM84413.1; -.
PIR; AC0408; AC0408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deng W., Burland V., Plunkett G. III, Boutin A., Maylerna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C. Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G Straley S.C., McDonough K.A., Nilles M.L., Matson J.S.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP cytidylyltransferase) (MCT).
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                                                                                                                                                                                                                       HAMAP; MF_00108; -; 1.
InterPro; IPRO1228; ISPD_synthase.
Pfam; PF01128; ISPD; 1.
PIRSF; PIRSF006765; DPCME_synth; 1.
TIGRPAMS; TIGR00453; ispD; 1.
PROSITE; PS01295; ISPD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Yersinia pestis KIM.";

7. Bacteriol. 184:4601-4611(2002).

-i- FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-20-methyl-D-erythritol from CTP and 2C-methyl-D-erythritol 4-
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STATUS / Biovar Mediaevalis;
Phihmed=12142430
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IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK
                                                                 AVVPAAGVGKRMQADRPKQYLFLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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                                 AVLPAAGIGSRMLVDCPKQYLTVGGKTIIEHAIFSLLHHPRIQRVIVVIHPQDTQFSRLS
                                                                                                    Conservative
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Pred. No. 1.2
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Matches 107
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HAMAP; MF 00108; -; 1.

InterPro; IPR001228; ISPD_synthase.

Pfam; PF01128; IspD; 1.

PIRSF; PIRSF006765; DPCME synth; 1.

TIGR0453; ispD; 1.

PROSITE; PS01295; ISPD; 1.

Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-entities.
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2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
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16-OCT-2001
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28-FEB-2003 (Rel. 41, Last annotation
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mplete genomic sequence of Pasteurella multocida Pm70.";

oc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-
METHYL-D-ERYTHRITOL FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-
PHOSPHATE (BY SIMILARITY).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = 4-(cytidine 5'-diphosphol-2-C-methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third stel.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third stel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lyltransferase) (MCT).
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                                                                                                                                                                                                                                                    Similarity
                                 IAKHPDIITAPGGKERADSVLSALKALEDIA--SENDWVLVHDAARPCLTGSDIHLQIDT 126
                                                                                                                                       AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
LLTHPKIQLVEGGSSRADSVLNGLNAVKSAVQNSEDFWVMVHDAARPCLTHQDLDKLVQV 133
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                                                                                                            AVVPAAGIGSRMQMDKEKQYLHIHGKTILEHTLSVLLGYPLIEKIILAVAANDPYISTCP
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                                                                                                                                                                                                                                                                                                                                      238 AA;
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                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                    Score 505;
Pred. No. 5
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.4e-37;
                                                                                                                                                                                                                         79;
                                                                                                                                                                                                                                                                            Length 238;
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BUCAI
ISPD E
                                                                                                                                                                                                                                                                                                                                             Complete proteome. SEQUENCE 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Q46893; 1152.
HAMAP; MF_00108; -; 1.
InterPro; IPR001228; ISPD_synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P57495;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-DCT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEE
                                                                                                                                                                                                                                                                                                                                                                                                 TIGRPAMs; TIGRO0453; ispD; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01128; IspD; 1.
PIRSF; PIRSF006765; DPCME_synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytidylyltransferase) (MCT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP001119; BAB13118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Buchmera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buchnera aphidicola (subsp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-
METHYL-D-ERVITHRIFOL FROM CIP AND 2C-METHYL-D-ERVITHRIFOL 4-
PHOSPHATE (BY SIMILARITY).
CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate =
diphosphate + 4-(Gytidine 5'-diphospho)-2-C-methyl-D-erythritol.
PATHMAY: Nonmevalonate terpenoid blosynthesis pathway; third step
SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUCAI
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73
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ISSNPRIISVVGGEKRINSVLSGLIVVKNV----DWVIVHDAVRPCLSYKDLEKLISIIK
                                                    IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                               AIVPAAGIGSRMKIDVPKQYIKIQNRTILEHTLTTLLHPNIVQIIVSLNKKDNYFHKLS
                                                                                                                                                                AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                             26922 MW;
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                                                                                                                                                                                                                                                          39.6%;
44.4%;
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                                                                                                                                                                                                                                                          Score 474.5;
Pred. No. 2.5
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                                                                                                                                                                                                                                                                                                                                             3E8AFDEF35BCB706 CRC64;
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                                                                                                                                                                                                                              .5e-34;
les 67;
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                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                        237;
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                                                                                                                                                                                                                                 Gaps
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NDPVGGILALSSHDTLKH--VDGDTITATIORKHVWRALTPQMFKYGMLRDALQR-TEGN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB063522; BAC24678.1; -. HAMAP; MF_00108; -; 1. InterPro; IPR001228; ISPD_synt
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
(4-diphosphocytidyl-C-methyl-D-erythritol synthase) (MEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8D223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01128; IspD; 1. TIGKFAMS; TIGR00453; IspD; 1.
PROSIT3; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the endocellular obligate symbiont flies, Wigglesworthia glossinidia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Akman L., Yamashita A., Watanabe
Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=36870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wigglesworthia glossinidia brevipalpis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytidylyltransferase) (MCT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-2C-methyl-D-erythritol from CTP and 2C-methyl-D-erythritol 4-phosphate (By similarity).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospha)-2-C-methyl-D-erythritol.

PATHMAY: Nonmevalonate terpenoid biosynthesis pathway; third step. SIMILARITY: BELONGS TO THE ISPD FAMILY.
186
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                                                                                                                                                                                                                                                                                                                                  97;
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                      LKNKKINIVIGGKSRTESVISALK----FVSKVDWVLVHDAVRPCLHKNDLNKLLKVINI 125
                                                                                                                                                                                                                                                                     VVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELSI 69
                                                                                                                                            AKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLKN 129
                                                                                                                                                                                                            if PAAGIGKRMGYKYPKQYIKIKNKTILEHSISLFIDKIYVKXILIAINKKDYWPKLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISVIDEASALEYCGYNPLLVLGSCRNIKITWPEDLVLANFYLK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYME 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNEVGAILAREVSDTIKYSNIKQKKAVYTVYRKNIWHALTEQIFQVELIKNCIKKIIKDQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32:402-407 (2002)
                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     26240 MM;
                                                                                                                                                                                                                                                                                                                        38.6%; Score 462.5; DB 1;
44.3%; Pred. No. 2.6e-33;
Mismatches 74;
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_00108; -; 1.
InterPro; IPR001228; ISPD; 1.
Pfam; PF01128; ISPD; 1.
PIRSP; PIRSP006765; DPCME synth; 1.
PIGRFAMS; TIGR00453; ispD; 1.
PROSITTS; P801295; ISPD; 1.
PROSITTS; P801295; ISPD; 1.
PROSITTS; P801295; ISPD; 1.
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SEQUENCE 236 AA; 26967 MM; B3CCB1F88740DD25 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379(2002).

Science 296:2376-2379(2002).

-!- FUNCTION: Catalyzes the formation of 4-diphosphocytidy1-2C-aethyl-D-erythritol from CTP and 2C-methyl-D-erythritol 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ?hosphate (By similarity).
-!- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate =
diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol
-!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third st
-!- SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electronic Control of the Electroni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60) (4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE014116; AAM67955.1; -.
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CBI_TaxID=98794;
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                                                                                                                                                                               66 NFFQKLSISSDLRVFSVLGGNERIHSVLSGL----IITTDAKWVIIHDAVRPCLSYQDLE 121
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   QR-TEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQ 229
                                                            NLIAITKNTKVGGILARPVCDTIKYSNRKNKTILHTIPRNQLWHALTPQLFPINLLRFCL
                                                                                                               LOIDTLKNDPVGGILALSSHDTLKHVD--GDTITATIDRKHVWRALTPQMFKYGMLRDAL 179
                                                                                                                                                                                                                                     PYWPELSIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIH
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.2%;
43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 457.5; DB 1
Pred. No. 7.5e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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g, 182 KKIVEDKINITDEASALSYCGYHPLIVLGSYKNIKITYPEDLIFAEFYLKE 232

Search completed: January 29, 2004, 15:50:40 Job time : 5.34994 secs

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Result
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Listing first 45 summaries
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Q8dc60 vibrio vuln
Q8fej 5 escherichia
Q8ebr2 shewanella
Q8ebr2 shewanella
Q8d223 wiggleswort
Q9eyy4 klebsiella
Q64726 arabidopsis
Q8d191 synechococc
Q48230 haemophilus
Q48154 haemophilus
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		Q8cjx6 streptomyce	Q9uzi7 pyrococcus	Q8czf5 yersinia pe		Q98cm6 rhizobium l	Q9x364 bacillus an	Ŋ	Q9cd44 mycobacteri	Q8g5pl bifidobacte		Q9cef8 lactococcus	Q8i273 plasmodium		Q8br14 mus musculu			0		Q8nyi0 staphylococ			Q8dpi2 streptococc			Q8cq77 staphylococ	Q8g7e2 bifidobacte		Q8e4b4 streptococc

ALIGNMENTS

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130 SHETGGILATPVRDTMKRANAQQMIDHTVDRNALWHALTPQMFKAEVLTDALSDALAQGV 189	129 NDPVGGILALSSHDTLKHVDG-DTITATIDRKHVMRALTPQMFKYGMLRDAL-QRTEGNP 186	70 IAQHDDIVRVAGGKERADSVLSALRFLSLQQQKADWVLVHDAARPCVAHQDIDALIERCS 129	69 IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128	ADRPKQYLQIHGKTILEHTIERLLSHPAITQVVVAVSI	9 AVVPAAGVGKRWQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS 68	Query Match 50.5%; Score 605; DB 16; Length 237; Best Local Similarity 55.4%; Pred. No. 9.6e-44; Matches 124; Conservative 31; Mismatches 67; Indels 2; Gaps 2;	COMPLECE PROCEOME. SEQUENCE 237 AA; 26005 MW; 35D0952D12B47ECD CRC64;		(DEC-2002) to the EMBL/GenBank/DDBJ d	"Complete genome sequence of Vibrio vulnificus CMCP6.":	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	STRAIN=CMCP6;	SEQUENCE FROM N.A.		NOBI marinego.	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;	Vibrio vulnificus.		cytidy1-2-methy1-D-er	01-MAR-2003 (TEMBLIE). 23, Last annotation update)	(Transmitted 23 Last semions	01-MAR-2001 (Transfrol 23 (Treated)	CBDC60 PRELIMINARY; PRT; 237 AA.	.6 0	ILT 1

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RESULT 3
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4-diphosphocytidyl-2C-methyl-D-erythritol synthase.
ISPD OR S03438.
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MEDLINE=2238234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J.,,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
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EMBL, AE015765; AAN81763.1; -
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01-MAR-2003 (TrEMBLrel 23,
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                                     SEQUENCE FROM N.A
STRAIN=MR-1;
                                                                                                                     Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                         Shewanella oneidensis.
Bacteria; Proteobacteria;
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Enterobacteriaceae; Escherichia.
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2-C-methyl-D-erythritol
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   PubMed=12368813;
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Pred. No. 1.6e
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Matches 106
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                                                                                                                                                                                                     "Genome sequence of the endocellular obligate flies, Wigglesworthia glossinidia."; Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24678.1; -. Complete proteome.
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Wat. Biotechnol. 20:1118-1123(2002).
EMBL, AB015780; AAN56435.1; -.
                                                                                                                                                                                                                                                                                            Akman L.,
Aksoy S.;
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NCBI_TaxID=164609;
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                                                                                                                                                                                                                                                                                                               Yamashita A.,
                                                                                                                                                                                      229 AA; 26240 MW;
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48.0%; Pred. No. 4
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                                                                                                                                 Score 462.5;
Pred. No. 1.
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Best Local S
Matches 62
O64726, Q91L91;
O64726; Q91L91;
O1-AUG-1998 (TERMELrel. 07, Created)
O1-JUN-2002 (TERMELrel. 21, Last sequence update)
O1-JUN-2003 (TERMELrel. 23, Last annotation update)
Putative sugar nucleotide phosphorylase
(4-Diphosphocytidy1-2C-methy1-D-erythritol synthase)
(2-C-methy1-D-erythritol 4-phosphate cytidyltransferase).
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Pfam; PP01128; ISPD; 1.
PROSITE; PS01295; ISPD; 1.
NON_TER 132 132
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J. Bacteriol. 0:0-0(2001).
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Last annotation update)
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Pred. No.
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RESULT QBDL91 ID OF AC OF DT 01

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Pfam; PF01128; ISpD; 1
Pfam; PTGR00453; /
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                                                                                                                                                                                                                                                                                                                    TIGREAMS; TIGRO0453; 15P
PROSITE; PS01295; ISPD;
Transferase.
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**EDLINB=20300921; PubMed=10841550;

**REDLINB=20300921; PubMed=10841550;

*Robdich F., Wungsintaweekul J., Eisenreich W., Richter G.,

*Schuhr C.A., Hecht S., Zenk M.H., Bacher A.;

*Biosynthesis of terpenoids. 4-diphosphocytidyl-2C-methyl-D-erythritol

*Synthase of Arabidopsis thaliana.";

*Synthase of Arabidopsis thaliana.";

*Proc. Natl. Acad. Sci. U.S.A. 97:6451-6456(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okada K., Kawaide H., Kuzuyama T., Takagi M., Seto H., Kam
"2-C-methyl-D-erythritol 4-phosphate cytidyltransferase.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (NOV-2002) to t
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AK118110; BAC42737.1; -.
Q46893; 1INJ.
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AC004136; AAC18936.2; -.
AF230737; AAF61714.1; -.
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                                                                                                                                                                                                               VVPAAGVGKRMQADRPKQYLPLAGKTVIEH----TLTRLLESDAFQKVAVAISVEDPY---
ELVKSEG-LEVTDDVSIVEYLKHPVYVSQGSYTNIKVTTPDDLLLAERILSEDS
                                                                                                                                                -WPELSIAKHPDIITAPGGKERADSVISALKALEDIASENDWVLVHDAARPCLTGSDIHL 122
                  -LQRTEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
                                                                                                                                                                                   ILLAGGOGKRMKMSMPKQYIPLLGQPIALYSFFTPSRMPE-----VKEIVVVCDPFFRD 135
                                                           -- KVLKDGSAVGAAVLGVPAKATIKEVNSDSLVVKTLDRKTLWEMQTPQVIKPELLKKGF
                                                                                                                                                                                                                                                                                                                                                                                    IPR001228; ISPD_synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Columbia;
                                                                                                                                                                                                                                                                                                          302 AA;
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                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                            33937 MW;
                                                                                                                                                                                                                                                           23.6%;
                                                                                                                                                                                                                                                                                                                                                        ispD; 1.
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:he EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakurai
                                                                                                                                                                                                                                                             Score 283.5; DE
Pred. No. 4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A., Narusaka
                                                                                                                                                                                                                                                                                                            7881DC5C8CB37B06 CRC64;
                                                                                                                                                                                                                                                Mismatches
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ka M., Carninci P.,
                                                                                                                                                                                                                                                                            DB 10; Length
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                                                                                                                                                                                                                                                                              302;
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RESULT
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Matches 80
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium"
                                                                                                                                                                                                       "Region II of Haemophilus influenzae type b capsulation locus involved in serotype-specific polysaccharide synthesis."; mol. Microbiol. 15:107-118(1995).
                                                                                                                                                                                                                                                                             MEDLINE=95272382; PubMed=7752885; van Eldere J., Brophy L., Loynds B., Hancock I., Carman S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyrophosphorylase.
Haemophilus influenzae
        encodes
                                                     Follens A., Ve
                                                                                                                                 STRAIN=RM135
                                                                                                                                                                                                                                                                                                                                                                   STRAIN=RM135;
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                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q48230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q48230
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                   MEDLINE=99194706;
                                                                                                                                                         SEQUENCE FROM N.A.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4-Diphosphocytidyl-2C-methyl-D-erythritol synthase.
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                          of Haemophilus influenzae type a Capsulation Locus Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPAAGMGKRMGASHNKLRLQLLGKPLLAWTLAAVAAAEAIEWIGVIGQPEDFPIWEALL
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                                                                              94706; PubMed=10094675;
Veiga-da-Cunha M., Merckx R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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     ribulose 5-phosphate
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sphate reductase/CDP-ribitol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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No. 2.
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hes 97;
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        reductase-CDP-ribitol
                                                                              Schaftingen
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Best Local
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                                                                                                                                                                                    MEDLINE=99194706; PubMed=10094675;
MEDLINE=99194706; PubMed=10094675;
Veiga-da-Cunha M., Merckx
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
Bifunctional ribulose 5-phosphate reductase/CDP-ribitol
                                                                                                                                                                           Pollens A., \van Eldere J
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01-NOV-1996
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Follens
                       STRAIN=ATCC 9006;
                                            SEQUENCE FROM N.A
                                                                                                         pyrophosphorlase
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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NCBI TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
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                                                                                      Bacteriol.
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- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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                                                                                                                                                      of Haemophilus
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Pred. No. 7
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Pfam; PF01128; ISpD; 1.
Pfam; PF01128; ISpD; 1.
PROSITE; PS00061; ADH_SHORT; 1.
Oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AB011288; AAN48247.1; -. Nucleotidyltransferase; Transferase; Complete proteome.
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InterPro; IPR001228; ISPD_synt)
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                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                TEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFY
                                                                                                                                                                                ESICASYLENEDRI-VQGGENRHSSMLCGLSVLD--FKDEDIILVHDAARPFVLADBLDS
                                                                                                                                                                                                                                                                          YVLILAGGTGSRMGSKIPKOFLELNGEPILIHSLKR-FONWGKOKRIVLVSHFESI-PKI
                                                                                                                                                                                                                                                                                                                      WAVVPAAGVGKRWQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            474 AA;
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                            SIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               26662 MW;
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                                                                                                                                                                                                                                                                                                                                                                                          21.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Complete proteome. 62 MW; C02400F042434DFB CRC64;
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TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spirochaetales; Leptospiraceae; Leptospira
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                                                                                                                                                                                                                                                                                                                                                                  48;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                Score 256; DB
Pred. No. 6.5e-
48; Mismatches
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Pred. No. 1.1e-13;
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                                                                                     SFLDREHVWFMKTPQGIRGDVLKELLTFS
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RESULT 12
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Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanam M.J.,
Paugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Palson W.C., Ayodeji B., Kraul M., Shetty J., Walek J., Van Aken S.E.
Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
"The Brucella suis genome reveals fundamental similarities between
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
2C-methyl-D-erythritol 2,4-cyclodiphosphate
synthase/4-diphosphocytidyl-2C-methyl-D-erythritol synthase.
MEDLINE=21877339; PubMed=11882717;
Lazarevic V., Abellan F.X., Beggah S.,
"Comparison of ribitol and glycerol te
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Brucellaceae; Brucella.
MCBI_TaxID=29461;
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Bacteria; Firmicutes;
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Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
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18; Mismatches 9
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S., Karamata D.,
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EMBL, AJ313428; CAC86109.1; -
InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; ISPD; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase.
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STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

STRAIN=YS-314 / Yemazaki J., Hino Y., Kikuchi H.,

Kawarabayasi Y., Yemazaki J., Hino Y., Kikuchi H.,

Ikeo X., Suguki M., Mashima J., Itoh T., Yamagishi

Usuda Y., Sugimoto S.;
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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SEQUENCE 248 AA; 26727 MW; AC66FF5894BCEFF3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 HTKDILKKFIGQDDRLVVVEGGSDRNESIMSGIRYIEKEFGIQDNDVIITHDSVRPFLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70;
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                                                                                                                                                                                                                                                                                                 Similarity
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  HLQIDTLKNDPVGGIL-ALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDAL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHQQ 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MFKYGMLRDALQR--TEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFY
                                                        LTRRGLLNDPEGVRVRLVHGGGERADSVWAGLQAID---HDDAIVLIHDSAR-ALTPPGM
                                                                                                         ----SIAKHPD---IITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDI 120
                                                                                                                                                                                                                  AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE-DPYWPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFRISKLVELYNKLSDEQKAVLTDACKICSLAGEKVKLVRGEVFNIKVTTPYÐLKVANAI
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                                                                                                                                                               ALLAAAGRGTRIGGPIPKAFVTLRGRSLVERSLRAMLTSEVVDEVIILVSPDMEDYAREL
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                                                                                                                                                                                                                                                                        Conservative
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                               20.7%;
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28.7%;
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                                                                                                                                                                                                                                                                     Score 248.5; DB
Pred. No. 3e-13;
7; Mismatches
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Pred. No. 2.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBO3F2F41D6CE5AB CRC64;
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                                                                                                                                                                                                                                                                                                                        DB 16;
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                                                                                                                                                                                                                                                                     93; Indels
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                                                                                                                                                                                                                                                                                                                        Length
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A., Nishi
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Baquero F., Berche P., Bloecker H., Brandt P., Chakrabortty T.,
A Baquero F., Berche P., Bloecker H., Brandt P., Chakrabortty T.,
A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
A Bantier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Madueno E., Maitournam A., Mata Vicente J. Ng E., Nedjari H.,
A Madueno E., Maitournam A., Mata Vicente J. Ng E., Nedjari H.,
A Madueno E., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Machiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
A Vacquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
A "Comparative genomics of Listeria species.";
EL Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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01-MAR-2002 (TrEMBLrel. 20, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical protein lmo1086.
LM01086.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01295; ISPD; 1.
Hypothetical protein; Complete
SEQUENCE 236 AA; 26712 NW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ListiList; LMO01086; -. InterPro; IPR001228; ISPD_synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8Y832;
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes
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                                                                                                                                                             VQER 233
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                                                                                                                                                                                                                                                                                                                                              -----YGMLRDALQRTEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFY 226
                                                                                                                                                                                                                                                                                                                                                                                                                 ENIDM---
                                                                                                                                                                                                                                                                                  TIQKHYNNLTD-----DEKQILTDACKICLLAGEKVKLVNGGISNIKITTPYDLKVANAI
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                                                                                                                                                                                                                                                                                                                                                                                                             ---ALEFGSVDTVIPAVDTIVESTNHDFITDIPVRGNIYQGQTPQSFNMK 174
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6712 MW; ACD3CB124E9A5098 CRC64;
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Pred. No. 4.6e-13;
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RE SEQUENCE FROM N.A.

RC STRAIN=TLS / ATCC 49652 / DSM 12025;

RX MEDLINB=22103685; PubMed=12093901;

RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

RA Eisen J.A., Nelson K.E., Paulsen I.T., Nelson W.C., Haft D.H.,

RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

RA HOlt I., Umayam L.A., Mason T., Brenner M., Shea T.B., Parksey D.,

RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

"The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).

BR TIGR; CT1317; -...

DR TIGR; CT1317; -...

DR TIGR; CT1317; -...

DR TIGR; CT1317; -...

DR FAmm, PF01128; ISPD; 1.

DR PROSITE; PS01295; ISPD; 1.

DR PROSITE; PS01295; ISPD; 1.

DR Complete proteome.

SSQ SEQUENCE 246 AA; 27022 MW; DSDA46B55C2F5A56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8KCU3;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidyl-2C-methyl-D-erythritol synthase.
ISPD OR CT1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBI_TaxID=1097;
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85
9.
                                                                                                                               179
                                                                                                                                                                   126 D-DIARLSATHGACVPATKPKDTIKYVGCNPEIFGETLDRSRLLQVQTPQGPAPAKLIEA
                                                                                                                                                                                                               121 HLQIDTLKNDPVGGILALSSHDTLKHV--DGDTITATIDRKHVWRALTPQMFKYGMLRDA 178
                                                                                                                                                                                                                                                          66 IAKANGFTKITAIIEGGKERQDSIGNCMKLIEQEIENSGVMPDAILVHDGARPFIQPEEI
                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                10 VVPAAGVGKRMQAD--RPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVED-PYWPE 66
                                                                                                                                                                                                                                                                                                                                            6 IIAASGVGKRMKLDGGRSKOMLEIGGQPVIWHTMKAFQEASTVESVYIATLPDSIPVFKE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                    76;
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 33.0
76; Conservative
                                                                                                                                                                                                                                                                                                LSIAKHPDIITA--PGGKERADSVLSALKALEDIASEN----DWVLVHDAARPCLTGSDI 120
                                                                                 -HRLAGEEQWYATDDAALVERYFPQQAIRIYETGYHNIKITTPEDVFIGE 233
                                                                                                                      LQRTEGNPA--VTDEASALELLGHKP--KIVEGRPDNIKITRPEDLALAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                           19.4%; Score 232:5; DB 16; Length 246; 33.0%; Pred. No. 6.9e-12; tive 39; Mismatches 98; Indels 17;
                  2004, 15:54:06
                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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1516
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11:
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                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*
/cgn2_6/ptodata/1/pubpaa/US07
:/cgn2_6/ptodata/1/pubpaa/US06
:/cgn2_6/ptodata/1/pubpaa/US06
:/cgn2_6/ptodata/1/pubpaa/US06
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/cgn2_6/ptodata/1/pubpaa/US09A PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09E PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09E PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10E NEW PUB.pep:*
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6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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6/ptodata/1/pubpaa/USO8_I
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/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                          NEW PUB. pep: *
PUBCOMB. pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, 18 derived by analysis of the total score distribution

SUMMARIES

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0	1 UT	572	572	580.5	582	582	584	584.5	616	620	638	1516	1516	1516	Score
35.2	36.7	37.7	37.7	38.3	38.4	38.4	38.5	38.6	40.6	40.9	42.1	100.0	100.0	100.0	Query Match I
266	213	270	270	298	276	276	294	280	283	279	279	285	285	285	Query Match Length DB
7	2	5	7	12	12	12	12	12	12	12	12	11	10	10	8
US-10-369-493-8419	US-10-369-493-19675	US-10-369-493-9359	US-10-369-493-9184	US-10-369-493-17751	US-10-369-493-16082	US-10-369-493-15690	US-10-369-493-15324	US-10-369-493-21079	US-10-369-493-802	US-10-369-493-201	US-10-369-493-13766	US-09-941-947A-12	US-09-934-868-74	US-09-934-903-8	ID
Sequence 8419, Ap	Sequence 19675, A	Sequence 9359, Ap	Sequence 9184, Ap	Sequence 17751, A	Sequence 16082, A	•	Sequence 15324, A	Sequence 21079, A	Sequence 802, App	Sequence 201, App	Sequence 13766, A	Sequence 12, Appl	Sequence 74, Appl	Sequence 8, Appli	Description

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813 990	314 575	238	99	141	245	311	271	295	268	240	306	315	261	261	261	261	292	311	297	295	316	287	257	289	269	289	284
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-10-108	-242-1 4-047-	-09-88	-10-264-213-	-10-289-7	0-369-493-	-09-738-626-	69-493-302	-10-3	US-10-369-493-65	9-49	US-09-712-363-186	60	9-493-1515	467	US-10-369-493-14419	US-10-369-493-11764	US-10-264-213-241	8-7131	US-10-156-761-11123	US-10-369-493-12283	US-10-369-493-20265	-10-369-4	US-10-369-493-9660	US-10-369-493-23046	US-10-369-493-7851	US-10-369-493-16541	US-10-369-493-9956
Sequence 3901, Ap Sequence 2568, Ap	10963,	(D)	e 208, ‡	e 1236	10645,	æ	æ	e 168	æ	e 17829	e 186, ?	Sequence 2607, Ap	æ	Ø	æ	Sequence 11764, A	e 241	Sequence 8, Appli	መ	Sequence 12283, A	æ	ው	9660,	e 23046,	e 7851,	Sequence 16541, A	•

ALIGNMENTS

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US-09-934-903-8
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 285
                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09934903 Patent No. US20020102690A1 GENERAL INFORMATION:
                                                                                                                                          Matches 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: CL1646 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: September 1, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KOffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andreas J.
APPLICANT: No. US20020102690Alton, Kelley C.
APPLICANT: Tomb, Jean-Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Methylomonas 16a
FEATURE:
61 NPISGVPEQDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNR 120
                                                                       1 MDYAAGWGERWPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLIFEHPVDDGRVTLR 60
                                               MDYAAGWGERWPAPAKINLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rouviere, Pierre
                                                                                                                                          Conservative
                                                                                                                                     100.0%; Score 1516; DB 10; 100.0%; Pred. No. 5.7e-156; tive 0; Mismatches 0;
                                                                                                                                          Indels
                                                                                                                                                                                    Length 285;
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RESULT 3
US-09-941-947A-12
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                                                      Sequence 12, Application US/099
Publication No. US20030003528A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Odom, James M
APPLICANT: Schenzle, Andreas J
APPLICANT: Schenzle, Andreas J
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1596 US NA
CURRENT PELICATION NUMBER: US/09/934,868
CURRENT FILING DATE: 2001-09-22
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
SEQ ID NO 74
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 285; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 74, Application US/09934868 Patent No. US20020137190A1
APPLICANT: Brzostowicz, Patricia C. APPLICANT: Cheng, Qiong APPLICANT: DiCosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Methylomonas 16a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                        GACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSALYKKLEQG 285
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                                                                                                                                                                                                                                                              TGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDYAAGWGERWPAPAKLNIMIR I TGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTIR
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Pred. No. 5.7e-156;
Mismatches 0;
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Sequence 13766, Application US/10369493
Fiblication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
FITTE OF INVENTION: EXAMPLESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXAMPLESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13766
LENGTH: 279
TYPE: PRT
ORGANISM: Pseudomonas fluorescens
US-10-369-493-13766
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CURRENT FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
VUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
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Best Loc
Matches
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Best Local Similarity
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                                         Query Match
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APPLICANT:
APPLICANT:
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APPLICANT: ROUVIETE, Pierre B.
TITLE OF INVENTION: CAROTEMOID PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REFERENCE: CL1903 US NA
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ORGANISM: Methylomonas 16a
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Local Similarity
nes 135; Conserv
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Odom, J. Martin
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Conservative
  42.1%; Score 638; DI
49.6%; Pred. No. 1.20
1tive 41; Mismatches
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  DB 12;
1.2e-60;
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RESULT 6
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US-10-369-493-201
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; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-201
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Best Local Similarity
Matches 132; Conserv
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 201
LENGTH: 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILB REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                       245
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                                                                                     FGEFESPASARKVÍNQAPEWMQGFVÁRGVNISPÍH 279
                                                                                                                                                                        PTDPELKRNSPIRTLPALLQAPFKNDCEPIARKRFREVEQLLSWLLEYTPSRLTGTGACV
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH INPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2003-02-21
J. NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 802
JEBRGTH: 283
TYPE: PRT
; CRGANISM: Xenorhabdus
US-10-369-493-21079
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US-10-369-493-802
                                                                        SEC ID NO 21079
LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21079, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 ($2052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-29
PRIOR FILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-03-41
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Best Local Similarity
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Publication No. US20030233675A1
                            CRGANISM:
                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 PVIFKDPELPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 GEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 WGLGLSKRELMDLGLRLGADVPVPVPGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 ACVFAQFCNKEDABSALEGIKDRWI-VFLAKGINQSALYKKI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 WQCGLSMDELAEMGLTLGADVPVFVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 QWPSPAKLNIFLYITGQRADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPVEGVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACVFAEFDTESEARQVLEQAPE-WLNGFVAKGANLSPLHRAM 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
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                         nematophilus
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Query Match Best Local Similarity

38.6%; 45.3%;

Score 584.5; DB 12; Pred. No. 7.8e-55;

Length 280;

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RESULT 8
US-10-369-493-15324
; Sequence 15324, Application US/10369493
; Publication No. US20030233675A1
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US-10-369-493-15324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                 137
                                                                                                                                     197
                                                                                                                                                                                                                                                                                                                                                                                                                                                         126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         11 WPAPAKLNIMIRITGRREDGYHLLQTVFQMLDLCDWLTFHEVDDGRV-TLRNPISGVPBQ 69
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                                                                                            CNKEDAESALEGIKDRWIVFLAKGINQSALYKKIE 283
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                                                        ATRAAAEQAMAHLPGNLRAWVVEGAAHSPLLDALD 291
                                                                                                                                        <u>LTRDAAPAKIADFASGSLLDNAFÉPÝLRRREPAIEAVFQALSRIGTPRLTGSGSGCFVEF</u>
                                                                                                                                                                       LTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAI-DALLCYAEARLTGTGACVFAQF 248
                                                                                                                                                                                                                 TLAELGLRIGADVPVFVRGHNAWAEGVGEKLTPISLPQAAYVLVDPGIHVPTPVLFQSQB 196
                                                                                                                                                                                                                                                                                              DDLMYRAARALQIHAGTALGAELRVDKRIPAGGGFGGGSSDAATVLVALNALMGLGLPVD 136
                                                                                                                                                                                                                                                                                                                                  DDLTVRAANLLKSHTGCVRGVCIDIEKNIPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR 129
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; Pred. No. 9.5e-55;
42; Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 294;
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Query Match
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RESULT 9

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Score

582;

B

12;

Length 276;

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ORGANISM: Xanthomonas campestris
US-10-369-493-15690
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US-10-369-493-16082
US-10-369-493-16082
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SEQ ID NO 15690
LENGTH: 276
                                                               CURRENT APPLICATION UNBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION UNMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
IUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16082
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16082, Application US/10369493 
Publication No. US20030233675A1 
GENERAL INFORMATION:
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Blatex, Steven C.
APPLICANT: Slatex, Steven C.
APPLICANT: Slatex, Steven C.
APPLICANT: Chen, Xianfeng
FITE OF INVENTION: EXCRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FITE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
ERIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              EPELICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
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                  TYPE: PRT
ORGANISM: Xanthomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 ELMDIGLRIGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAEN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 LTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAI-DALLCYABARLTGTGACVFAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 TLABIGIRIGADVÞVFVRGHNÁMAEGVGEKITÞISIÞQAAYVLVDÞGIHVÞTÞVLFQSQE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 ATRAAAEQÁMAHLPGNLRAWVVEGAAHSPLLDAL
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46.0%; Pred. No. 1.4e-54;
                     campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Mismatches 105;
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US-10-369-493-17751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17751
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17751, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 132; Conservative
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 38.3%;
Local Similarity 46.3%;
                                                                                                                                                                                                                    130 ALMHTRLDVAVLAALGLRLGADVPVEVHGCNAMABGVGECLTEMILEGAAYLLLDEGVCV 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDYAAGWGERWPAPAKLALMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRV-TL 59
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                                                                      GTGACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSALYKKLE 283
                          GSGSGCFVEFSTRDEAECALERLPYGLCAWVADGASRSPLLDVLK 294
                                                                                                                                                                                                                                                                   RLWGLGLSKRELMDLGLRLGADVPVFVFGCSAWGBGVSEDLQALTLPEQWFVIIKPDCHV 179
                                                                                                                                                                                                                                                                                                                  GESVTGVVEADDLVVRAAYLLKYATNVHLGADIFVEKRIPVGGGFGGGSSDAATVLLVLN 129
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                                                                                                                     PTRELFLDPDLTRDASPATIGDFIAGTAFGNAFEPVLRRRESAVAGALDVLSEVGFARVT 249
                                                                                                                                                                                                                                                                                                                                                                                                                   VDDGVGW-SAWPAPAKLNIFIQITGRRVDGYHELQTVFRLLDWGDTIHLRVREDGQIHRI 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Mismatches 106; Indels
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Pred. No. 2.3e-54;
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1; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
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; ORGANISM: Xylella fastidiosa
US-10-369-493-9359
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US-10-369-493-9184
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LENGTH: 270
TYPE: PRT
                                                                                              NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9359
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9359, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                      APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Coen, Xianieng
TITLE OP INVENTION: EXPRESSION OP MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OP INVENTION: EXPRESSION OP MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OP INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
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                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OP INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OP INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE STERRICE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US(10/369,493)
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
                                                 TYPE: PRT
                                                                      ENGTH:
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Similarity 47.4%;
28; Conservative 4
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Pred. No. 1.7e-53;
12; Mismatches 98;
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CURRENT APPLICATION NUMBER: US/10/369,493;
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID MOS: 47374
SEQ ID NO 19675
LENGTH: 213
TYPE: PRT
ORGANISM: Nitrosomonas europaea
RESULT 15
US-10-369-493-8419
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US-10-369-493-19675

; Sequence 19675, Application US/10369493

; Publication No. US20030233675A1
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
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                                                                                                                LTRNTIPIKMAAFSMGQGHNDLEPVAMRM-QPV 212
                                                                                                                                                                                                                                                                                               DLCVRAAKLIRORFGRESLGVKIHLEKNIPLGGGLGGGSSDAATTLIALNRLWGINWKRE 120
                                                                                                                                                                                                                                                                                                                                        DLTVRAANLLKSHTGCVR-GVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR 129
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  Application US/10369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.7%; Score 556; DB 12; Length 213; 51.6%; Pred. No. 6.6e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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Search completed: January 29, Job time: 20.4547 secs
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; TYPE: PRT
; ORGANISM: Ralstonia metallidurans
US-10-369-493-8419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 8419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                      228 ALLCYA-BARLTGTGACVFAQFCNKEDAESALBGLKDRWLVFLAKGLNQSAL 278
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                                                                                            WIKNYSPHARMTGSGACVFARFEDEQTAQRVMERLPSEWDGRCVKSLSHHPL 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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49.1%; Pred. No. 2.4e-49;
tive 35; Mismatches 77;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.
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1516
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1736.455 Million cell updates/sec
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ALIGNMENTS

유	mery atch	Length	₽B	Ħ	scription
1516	100.0		23		High growth
1516	100.0	285	23	AAE22304	Methylomonas
1516	200.0	285	23	AAU80328	Methylomonas
624	41.2	281	24	ABP78450	W. gonorrhoe
616	40.6	283	21	AAB11374	E. coli YCHB
616	40.6	283	22	AAB68286	Amino acid s
332	21.9	283	23	ABP25586	Streptococcu
320	21.1	293	23	ABB50111	Listeria mon

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ABP38503

Staphylococcus

WPI; 2002-452200/48

Koffas M,

Odom JM,

Schenzle A;

S. pneumoniae type	0	24	289	٠	96	4.5
Streptococcus pneu	AAU37989	22	289	٠	96	4.5
Streptococcus pneu	AAU37651	22	289	٠	96	4. (2)
Streptococcus pneu	AAY81774	21	289		96	42
Enterococcus faeca	AAU35064	22	341		86	4 []
ate pa	AAB60866	22	331	6.5	98	40
llular	AAU34420	22	310	•	101	39
a t	AAU38118	22	309	•	105	38
-	on.	21	355	•	110	ų,
2.	8	22	231	7.3	110	36
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Ë	808	23	288	7.4	111.5	IJ A
st	AAG45151	2	370	7.5	114	<u>ယ</u> ယ
	AAG45152	2	246	7.5	114	3 2
818	AAG45153	21	244	7.5	114	ندا دا
H	AAW81016	20	483	7.6	115.5	u O
C	AAU35370	22	314	8.2	125	29
Ω	AAW98746	19	238	8.4	127	28
		22	746	9.2	140	27
	AAY37333	20	263	Ľ	176.5	26
sequen	AAY35818	20	141	11.7	178	25
thali	AAG12034	21	185	'n	195	24
thal	AAG12035	21	184	Ņ	195	20
Bifidobacterium lo	ABP65646	23	316		204.5	22
	AAB76645	22	311	4	216	21
C glutamicum prote	AAG90761	22	311		216	20
0	AAU54372	22	324	•	223	19
humar	ABG17595	22	360	4	224	18
Amino acid sequenc	AAB68285	22	405	7.	263	17
c	AAG81135	22	306	7.	267	97
abidopsis thali	AAB70487	22	383	.7	268	بر س
aliana ychB	AAB70486	22	316	7.	268	'U' F-1
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Rhodococcus erythr	AAE31685	24	311	ъ.	278	10

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RESULT 1
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                                                                                                                                                                                                                                                                                                             01-SEP-2000; 2000US-229858P.
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                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2001; 2001WO-US26827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The invention relates to a high growth methanotrophic bacterial strain, CC which grows on a Cl carbon substrate e.g. methane and methanol, and CC comprises a functional Embden-Meyerhof carbon flux pathway comprising a gene coding a pyrophosphate dependent phosphofrutokinase enzyme or a 16s CC RNA. The bacterial strain is useful for the production of single cell CC protein and for the biotransformation of a nitrogen-containing compound, CC e.g. ammonia, nitrate, citrite or nitrogen. It is also useful for the production of a feed product comprising a protein, carbohydrates and a CC pigment and for reducing oxygen demand, for removing nitrates and CC mitrites in methane-containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are CC present. The bacterial strain of the invention can be used as a CC denitrifying agent for the conversion of nitrate or nitrite to nitrous oxide with methane or methanol as a carbon source. It is also used in the CC production of biomass including proteins, carbohydrates and a wide variety of pigments (particularly for isoprenoid pigments for the CC purpose of generating animal feeds), in production of terpenoid and CC carotenoid compounds, useful as pigments and as monomers in polymeric CC sequences ABG61591-ABG61590 represent high growth methanotrophic CC bacterial strain porteins of the invention
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Best Local
                                                         Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; 4-diphosphocytidyl-2-C-methylerythritol kinase;
                                                                                                                                                   Methylomonas 16a sp. 4-diphosphocytidyl-2-C-methylerythritol kinase
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gle cell proteins, grows on a Cl carbon substrate, and comprises a
ctional gene encoding in Embden-Meyerhof carbon pathway
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Methylomonas 16a

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                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for producing carotenoid compounds. CC The method comprises a transformed metabolising host cell, comprising CC suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule conding an enzyme in the carotenoid biosynthetic pathway, under the CC control of regulatory sequences, and contacting the host cell with carbon consistent to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by cusing microorganism having a nucleic acid molecule encoding enzymes in CC using microorganism having a nucleic acid molecule encoding enzymes in CC using microorganism having a nucleic acid molecule encoding enzymes in CC using microorganism having a nucleic acid molecule particle suseful in CC diet, and aquaculture elements. The carotenoids are also useful as CC intermediates in the synthesis of steroids flavours and fragrances and CC compounds for potential electro-optic applications. The present sequence CC is Methylomonas 16a sp. 4-diphosphocytidyl-2-C-methylerythritol kinase CC (IspB) enzyme used in the invention.
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Matches 285;
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GACVFAQFCXKEDAESALEGLKDRWLVFLAKGLNQSALYKKLEQG
                               GACVPAOFCNKEDAESALEGLKDRWLVFLAKGLNOSALYKKLEOG
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100.0%; Pr
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Rouviere PE;
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Pred. No. 1.3e-155;
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                                                                                                                                                                                                                                                                                                                                                                                an isopremoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an isopremoid compound biosynthetic enzyme, and for the microbial production of isopremoid compounds. The molecules of the invention are also useful for regulating isopremoid biosynthesis in an organism and for producing recompanism for producing various isopremoid compounds. The nucleic acid is also useful for feed additive, for the production of keratenoids and their derivatives, isopremoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 4 (ORF4) ychB/ispE (4-diphosphocytidyl-2-C-methylerythritol kinase enzyme) protein of the invention, as described
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                         GACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSALYKKLEQG 285
                                                                       TGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGT
                                                                                                           LWGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVN
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                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP78450 standard;
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                                                                                                                                                                                                                                  MDYAAGWGERWPAPAKINIMIRITGRRPDGYHILQTVFQMLDLCDWLTFHPVDDGRVTLR
MIGSGACIFAAFQARNSAYNIYRQVSGLYEAYLAEGLSKHPL
                            LTGTGACVFAQFCNKEDAESALEGLKDRWLVFLAKGINQSAL
                                                  TAKIFTYEGLTRDSASSIMPTF---QNLQPFRNDMQAVVEKEYPEVMKAYSELSKYGSAM
                                                                                TGEIFSAENLTRNSAVVTMSDFLAGDN----RNDCSEVVCKLYRPVKDAIDALLCYAEAR 236
                                                                                                         WWQCGLTQWQLIDLGAALGADVPFFIFGKNAFASGIGKKLIGWDIPKQWYVIVKPPVHVS
                                                                                                                        LWGLGLSKREIMDLGLRLGADVFVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVN 180
                                                                                                                                                            NPVGGIPQEADLSYRAASLLQKYARNLAGVEIWLDKKIPTGAGLGGGSSDAATVLLVLNR
                                                                                                                                                                                                                 MNIADG-RQAFPAPAKLNIDIRITGRREDGYHNIESIFCLIDIQDTVYLKPRDDGKIILH
                                                                                                                                                                                                                                                                                                                         281 AA;
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                  Score 624; DB 24;
Pred. No. 7.1e-59;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel Escherichia coli genes (I) encoding proteins (II) designated YQCP, YHBC, YGGJ, YGBP, YCHB, YGBB, YVBB and WDTB, and genes (Ia) that encode orthologous gene products (IIa) in other microorganisms and which have antibacterial activity. Recombinant microorganisms in which expression of (I) or (Ia) can be regulated are used to identify compounds that bind to the gene products, particularly in affinity selection assays. (II) and (IIa) are used to identify, or prepare, antibodies and other proteins that bind to the gene products. Substances that bind to (II) or (IIa) are potentially useful as antibacterials for treating a wide range of infections in humans and animals. Sequences antisense to (I) and (Ia) can also be used as antibacterials. The specified genes are widely distributed in bacteria but have no close homologs in eukaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 23-24; 28pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Essential genes from bacteria, useful in screening for antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-639611/62
N-PSDB; AAC66044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agents, and related proteins, transformants
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ACVFAQFCNKEDAESALEGLKDRWL-VFLAKGLNQSALYKKL 282
                                                                                                                                                                                                                                                                                                                                                         DDLTVRAANLL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRL 121
                                                                                         PVIFKDPELPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                          QWPSPAKLNIFLYITGQRADGYHTIQTLFQFLDYGDTISIELRDDGDIRLLTPVEGVEHE 63
                                                                                                                                                 GEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTG
                                                                                                                                                                                                        WQCGLSMDELAEMGLTLGADVPVPVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
                                                                                                                                                                                                                                                                WGLGLSKRELWDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNT 181
                                                                                                                                                                                                                                                                                                                       DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RWPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 616; DB 21;
Pred. No. 5.3e-58;
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an isopentenyl monophosphate kinase (IPK) polypoptide. The enzyme is an isoprenoid biosynthesis stimulator. The IPK polynucleotide is useful recombinant production of IPK, as a source of probes, primers and antisense sequences and for increasing/reducing expression levels of IPK in cells, particularly of essential oil plants, so as to increase flow through the isoprenoid biosynthesis pathway, resulting in increased production of e.g. pigments, vitamins and essential oils, also to increase resistance to pests and pathogens and to improve plant strength. Nutant forms of the IPK polynucleotide can be used to express forms of IPK that are resistant to IPK-targeted herbicides, and recombinant IPK can be used to screen for antibiotics, herbicides and antimalarial agents directed against IPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding isopentenyl monophosphate kinase, useful e.g. for making transgenic plants with increased synthesis of isoprenoids, e.g. essential oils -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-308747/32
                                   182
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GEIFSAENLTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLIGTG
                                                                                          DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
                                                                                                                                                                                                                                                                           DDLTVRAANEL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 616; DB 22;
Pred. No. 5.3e-58;
9; Mismatches 96
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
                                                                                                                                                                                                                                                                                                                                                                                                                                          New Streptococcus protein for the treatment or prevention of or disease caused by Streptococcus bacteria, such as meningit for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                            Sequence
                                                                                                                         Streptococcus proteins.
                                                                                                                                                                                                                                                                                 activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 3188; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telford J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus polypeptide SEQ ID NO 348
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                                               Similarity
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                                                                                            283
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                               Conservative
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2000GB-0028727.
2001GB-0005640.
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                            58;
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                                             Score 332; DB 23;
Pred. No. 3.4e-27;
                            Mismatches 107;
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Ferez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
Rose M, Voss H;
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Daniels J, Goebe
Dominguez-Bernal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B12; bacterial infection; disease.
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                                                                                                                                                                                                                                                         C, Frangeul L, Couve E, Rusnick C, Fsihi H, Dehoux P
J, Chetcouani F, Nedjari H, Glaser P, Kunst F, Cossart
Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA,
Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A
J, Domann E, Hain T, Berche P, Charbit A, Durant L;
J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N,
De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
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Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides

Claim 6; SEQ ID No 2816; 192pp; French.

The present invention relates to the genome sequence of Listeria minocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, are antibodies, identification of L. monocytogenes and related organisms, are for biosynthesis and biodegradation, especially biosynthesis of Vitamin E12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and F 0

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                                                                                                                                           Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3348.
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                                                                                         Disclosure;
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08-NOV-1997;
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                                                                                   SEQ ID 3348; 267pp; English
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97US-064964P.
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Pred. No. 7.1e-26;
1; Mismatches 120
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open frame (ORF) nucleic acid sequences which encode the amino acid

reading sequences

Claim 4; Page 72-73;

85pp; English

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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                   useful for obtaining nucleic biosynthetic enzyme, and for altered activity -
                                                                                                          New nucleic acid molecule from Rhodococcus erythropolis AN12 strain, useful for obtaining nucleic acid encoding isoprenoid compound
                                                                                                                                                                                          N-PSDB; AAD48798.
                                                                                                                                                                                                                                                                        Bramucci MG,
Rouviere PE,
                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2001; 2001US-285910P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-2002; 2002WO-US15033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodococcus erythropolis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodococcus erythropolis ygbP (ispE) protein.
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Tao L, Thomas
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                                                                                                                                                                                                                                                                          Thomas SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme; ygbP;
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Pred. No. 6.5e-24;
1; Mismatches 103;
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RESULT 11
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            The present sequence represents an isopenteryl monophosphate kinase (II polypeptide. The enzyme is an isoprenoid biosynthesis stimulator. The IPK polynucleotide is useful recombinant production of IPK, as a source of probes, primers and antisense sequences and for increasing/reducing expression levels of IPK in cells, particularly of essential oil plants, so as to increase flow through the isoprenoid biosynthesis pathway, resulting in increased production of e.g. pigments, vitamins
                                                                                                                                                                                          New
                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel Rhodococcus erythropolis AN12 strain isoprenoid biosynthetic enzymes and polynucleotides encoding such proteins. Sequences of the invention are useful for regulating isoprenoid biosynthesis in an organism. They are useful for producing isoprenoid compounds and gene products having enhanced or altered activity. The present sequence is Rhodococcus erythropolis ygbp.
                                                                                                                                                                                                                                     WPI;
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                                                                                                                                                                       nucleic acid encoding isopentenyl monophosphate kinase, useful emaking transgenic plants with increased synthesis of isoprenoids.
essential oils, also to increase resistance
                                                                                                                                                            making transgenic plants essential oils -
                                                                                                                                                                                                                                   2001-308747/32.
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                                                                                                                               Page 52-53; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogen
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resistance; antibiotic; herbicide;
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e.g. pigments, vitamins
ce to pests and pathogens
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to improve plant strength. Mutant forms of the IPK polynucleotide can be used to express forms of IPK that are resistant to IPK-targeted herbicides, and recombinant IPK can be used to screen for antibiotics, herbicides and antimalarial agents directed against IPK.
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                                                                                                                                                                                          RВ,
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essential oil; pathogen r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQLDLSSKVDPLS-LLEKISTSGISQDVC 300
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                                                                                                                                                                                                                                                                                                                                                                                      sequence
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3; Mismatches
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Pred. No. 5.1e-21;
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                                                                                                                                                                                                                                                                                                                                                                 IPK;
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tance; antibiotic; herbic;
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                                                                                                                                                                                                                                                                                                                                                      herbicide;
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The present sequence represents an isopentenyl monophosphate kinase (II polypeptide. The enzyme is an isopremoid biosynthesis stimulator. The IPX polynucleotide is useful recombinant production of IPX, as a source of probes, primers and antisense sequences and for increasing/reducing expression levels of IPX in cells, particularly of essential oil plants, so as to increase flow through the isopremoid biosynthesis pithway, resulting in increased production of e.g. pigments, vitamins and essential oils, also to increase resistance to pests and pathogens

source

New nucleic acid encoding isopentenyl monophosphate kinase, useful e. for making transgenic plants with increased synthesis of isoprenoids,

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Example 8; Page 56-57; 62pp; English.

essential

oils

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ARBSULT 13
ARBSE21
ID ARBSE2
AC AABSE2
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The present sequence represents an isopentenyl monophosphate kinase (IP) polypeptide. The enzyme is an isopentald biosynthesis stimulator. The IPX polynucleotide is useful recombinant production of IPX, as a source of probes, primers and antisense sequences and for increasing/reducing expression levels of IPX in cells, particularly of essential oil plants, so as to increase flow through the isopremoid biosynthesis pathway, resulting in increased production of e.g. pigments, vitamins and essential oils, also to increase resistance to pests and pathogens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isopentenyl monophosphate kinase; IPK; isoprenoid biosynthesis; vitamin; essential oil; pathogen resistance; antibiotic; herbici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB68291;
                                                                                                                                                                                                                                                                  Example 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB68291 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIW )
                                                                                                                                                                                                                                                                                                                     nucleic acid encoding isopentenyl monophosphate kinase, useful making transgenic plants with increased synthesis of isoprenoi essential oils
                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-308747/32.
)B; AAF85084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRLDQTSNINPLT-LLENVTSNGVSQSIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENLTRNSAVVTMSDFLAGDNRNDCSEVVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APAKLNIMIRITGRRÞÞGYHLLQEVFQMLÐLCDWLTFH-PVDDGRVTLRNÞISGVÞ-EQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQDWSSEIGSDIPFFFSHGAAYCTGRGEIVQDLPPPFPLDLPMVLIKPREACSTAEVYKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383
                                                                                                                                                                                                                                                               Page 60-61; 62pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isopentenyl monophosphatase kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 275; DB 22;
Pred. No. 7.9e-21;
2; Mismatches 91;
                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cnesis; pigment;
herbicide;
                                                                                                                                                                                                                                                                                                                                                    isoprenoids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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Best Local S
Matches 91
                                                                                                                                                                21-SEP-1999;
11-OCT-1999;
05-NOV-1999;
                                                                                       Herz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and to improve plant strength. Nutant forms of the IPK polynucleotide can be used to express forms of IPK that are resistant to IPK-targeted herbicides, and recombinant IPK can be used to screen for antibiotics, herbicides and antimalarial agents directed against IPK.
                                            N-PSDB;
                                                                           Bacher A, Zenk M,
Herz S, Kis K, L
Wungsintaweekul J;
                                                                                                                                                                                                 04-AUG-1999;
21-SEP-1999;
                                                                                                                                                                                                                                   03-AUG-2000; 2000WO-EP07548
                                                                                                                                                                                                                                                         15-FEB-2001
                                                                                                                                                                                                                                                                                                                          genetic marker;
                                                                                                                                                                                                                                                                                                                                                         A. thaliana
                                                                                                                                                                                                                                                                                                                                                                                                    AAB70486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                         28-APR-2000;
                                                                                                                                                                                                                                                                                                   Arabidopsis thaliama
                                                                                                                                                                                                                                                                                                                       Isoprenoid biosynthesis; 2C-methyl-D-erythritol-4-phosphate;
genetic marker; plant; isoprenoid biosynthesis inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          AAB70486 standard;
                                                                                                                        (ZENK/)
                                                                                                                                   BACH/)
                                           2001-202774/20.
DB; AAF63675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                       ZENK
                                                                                                                                 BACHER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAHQPVAQLRQVLQSAGGLGTMMSGSGPSVFTLCREQAEAEQVLAIAKEKLNDPDVDFWL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNLAYRAAQLMINNFPQAHDN-YGGVDITLTKHIPMAAGLAGGSADAAAVLVGLDLLWNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APAKLNUMLRITGRRPDGYHLLQTVFQMLDLCDWLTF--HPVDDGRVTL-RNPISGVPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLSKREIMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQ---WFVIIK-PDCHVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLTRPELEQLAAQLGSDIPFCIGGGTAIATGRGEILD - - PLPDGNCFWVVLAKHRSIEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDLTVRAANIL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APAKINLFLEILGDRPDGFHELVMVLQSIALGDKITVRANGTDDIRLSCGDSPLAN--DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLYRPVKDAIDALLCYA--EARLTGTGACVFAQFCNKEDAESALEGLKDR-----WL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPWAYQTYRQKFGKNYLNDDQSQRARRKTIHAGPLLQGIQHRNPGQIASHIHNDLEKVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 AA;
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                                                                                                                                                         2000DE-1020996
                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                99DE-1036663.
99DE-1045174.
99DE-1045175.
99DE-1048887.
99DE-1053309.
                                                                                                                                                                                                                                                                                                                                                         protein without
                                                                                     Luettgen
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                 Bisenreich
                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.8%; Score 270.5; 30.3%; Pred. No. 1.86 tive 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GEIFSAENLTRNSAVVTM------SDFLAGDNRNDCSEVVC
                                                                                       Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                          316
                                                                                     h W, Feller
Rohdich F,
                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                         leader sequence
                                                                                     Fellermeier M, ich F, Sagner S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .8e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                     Fischer M, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                   Hecht
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Enzymes which operate in the alternative isoprenoid pathway downstream from 2C-methyl-D-erythritol-4-phosphate, useful for screening a chemical library for inhibitors of the biosynthesis of isoprenoids -

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isoprenoids. Herbicide resistant enzymes can be used to produce herbicide formation. Methods from the present invention can be used to produce herbicide resistant enzyme variants which can be incorporated into plants to confer selective herbicide resistant on the plants. The methods are also useful for controlling weed by cultivating crops containing herbicide-resistant genes in the presence of weed-controlling effective amounts of herbicides. The inhibitors are used for inhibiting the biosynthesis of isoprenoids in plants, bacteria or protozoa. The present sequence represents the Arabidopsis thaliana yould present invention. leader sequence, which is given in an example from the present invention.
04-AUG-1999;
21-SEP-1999;
21-SEP-1999;
11-OCT-1999;
05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes functional enzymes (I) which operate in the alternative isoprenoid pathway downstream from 2C-methyl.D-erythritol-4-phosphate. (I) can be used as isoprenoid biosynthesis inhibitor. The enzymes are useful for screening a chemical library for inhibitors of the biosynthesis of isoprenoids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2C-methyl D-erythritol-2,4-cyclopyrophosphate or 4-diphosphocytidyl-2C-methyl-D-erythritol-2-phosphate, or their salts are useful for screening for inhibitors of the biosynthesis of sopprenoids. Herbicide resistant enzymes can be used as genetic markers
                                                                                                         03-AUG-2000;
                                                                                                                                            15-FEB-2001
                                                                                                                                                                            WO200111055-A1
                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                Isoprenoid biosynthesis; 2C-methyl-D-erythritol-4-phosphate; herbicide; genetic marker; plant; isoprenoid biosynthesis inhibitor.
                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana ychB protein.
                                                                                                                                                                                                                                                                                                                                        04-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                            AAB70487;
                                                                                                                                                                                                                                                                                                                                                                                                            AAB70487 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 12a; Annex Ea; 194pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -diphosphocytidyl-2C-methyl-D-erythritol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 LMDLGIRIGADVPVFVFGCSAWGEGVSEDLQAITLP---EQWFVIIKPDCHVNTGEIFSA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DITVRAANILKSHTGCVRGVCIDIEKNIPMGGGIGGGSSDAATTIVVLNRIWGIGISKRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APAKLMIMIRITGRRPDGYHLLQTVFQMLDLCDWLTEH-PVDDGRVTLRNPISGVP-EQD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENLTRNSAVVIMSDFLAGDNRNDCSEVVC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLIIKALNLYRKKTGSNRFFWIHLDKKVPTGAGLGGGSSNAATALWAANELNGGLVTENE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPCKINVFLRITGKREDGFHDLASLFHVISLGGTIKFSLSPSKSKDRLSTNVQGVPVDGR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRIDQTSNINPLT-LLKNVTSNGVSQSIC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iQDWSSEIGSDIPFFFSHGAAYCTGRGEIVQDLPPPFFLDLPMVLIKPREACSTAEVYKR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316
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                                                                                                           2000WO-EP07548
                                                                                                                                                                                                                                                                                                                                        (first entry
                  99DE-1036663.
99DE-1045174.
99DE-1045175.
99DE-1048887.
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                                                                                                                                                                                                                                                                                                                                                                                                              383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 268; DB 22;
Pred. No. 3.5e-20;
2; Mismatches 92
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Search completed: January 29, 2004, 15:49:42 Job time: 28.0514 secs

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CC 2C-methy1-D-erythrito1,
CC 4-diphosphocytidy1-2C-methy1-D-erythrito1-2-phosphate or
CC 4-diphosphocytidy1-2C-methy1-D-erythrito1-2-phosphate, or their salts
CC are useful for screening for inhibitors of the biosynthesis of
CC are useful for screening for inhibitors of the biosynthesis of
CC isoprenoids. Herbicide resistant enzyme can be used as genetic markers
CC in any cell that is normally sensitive to the inhibitory effects of
CC produce herbicide resistant enzyme variants which can be incorporated
CC produce herbicide resistant enzyme variants which can be incorporated
CC into plants to confer selective herbicide resistant on the plants. The
CC containing herbicide-resistant genes in the presence of weed-controlling
CC effective amounts of herbicides. The inhibitors are used for inhibiting
CC the biosynthesis of isoprenoids in plants, bacteria or protozoa. The
CC present sequence represents the Arabidopsis thaliana ychB protein,
CC which is given in an example from the present invention.
                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the alternative isoprenoid pathway downstream from 2C-methyl-D-crythritol-4-phosphate. (I) can be used as isoprenoid biosynthesis inhibitor. The enzymes are useful for screening a chemical library for inhibitors of the biosynthesis of isoprenoids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzymes which operate in the alternative isoprenoid pathway downstream from 2C-methyl-D-erythritol-4-phosphate, useful for screening a chemical library for inhibitors of the biosynthesis of isoprenoids -
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Herz S, Kis K, Lo
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ettgen H, Rohdich F, Sagner S,
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, Schuhr CA;
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OM protein - protein search, using sw model
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-434-774-12
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US-09-434-774-236
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ALIGNMENTS FESULT 1 S-09-252-991A-30806 Sequence 30806, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS	3 US-08-477-346-66 Sequence	.5 4.8 514 1 US-08-190-802A-66 Seguence	.5 4.8 486 3 US-08-348-518C-2 Sequence	.9 462 4 US-09-328-352-4742 Seguence	4.9 590 4 US-09-134-001C-4390 Sequence	4.9 397 4 US-09-107-532A-5568 Sequence	4.9 221 4 US-09-107-532A-5984 Sequence	4.9 1891 2 US-08-804-198-6 Sequence 6	4.9 1891 2 US-08-804-227C-12 Sequence	4.9 392 2 US-08-998-208-33 Sequence	4.9 392 2 US-08-451-778A-33 Sequence	4.9 392 1 US-08-451-777A-33 Sequence	.5 5.0 472 3 US-08-476-509B-5 Sequence	.0 472 3 US-08-348-518C-5 Sequence	.5 5.0 390 4 US-09-252-991A-19993 Sequence	.5 5.0 551 3 US-08-886-886-15 Sequence	5.0 455 4 US-09-328-352-5626 Sequence	5.0 260 6 5223425-10 Patent No.
RELATING TO PSEUDOM	90	66	2, 1	47	4390,	5568,	59	6	12,	33,	u u	33,	5, Appl	'n	1999		5626	₹ •

	RESULT 2 US-09-434-774-6
	Qy 252 BDAESALEGIKDRWIVFLAKGLNQSALYKKIE 283
259	Qy 192 RNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACVFAQFCNK : :
191	Qy 132 MDIGIRIGADVPVFVFGCSAMGEGVSEDLQAITLPEQMFVIIKPDCHVNTGEIFSAENLT
131	Qy 72 LTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLMGLGLSKREL 131
71 79	Qy 12 PAPAKINIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQDD
0,	Query Match 44.1%; Score 668; DB 4; Length 294; Best Local Similarity 51.8%; Pred. No. 1.8e-65; Matches 141; Conservative 36; Mismatches 95; Indels 0; Gaps
	; NUMBER OF SEQ ID NOS: 33142 ; SEQ ID NO 30806 ; LENGTH: 294 ; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30806
	CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
TO PSEUDOMONAS	FRACEDE NO. 6551/95 FRACEDE NO. 6551/95 FREEDRATION: FREEDRAMTION: Rubenfield et al. FITTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FITTLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 FURNAMENT APPLICATION NUMBER: US/09/252 991A

Sequence 6, Application US/09434774A

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APPLICANT: Cange, Bernd M
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MUCHES KINASE, AND METHODS OF USB
FILE REFERENCE: wsur14448
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID MOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID MO 6
LENGTH: 283
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4670
LENGTH: 283
TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: GATY L. BRECON et al.
APPLICANT: GATY L. BRECON et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
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Best Local Similarity
                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Patent No. 6562958
                                                                                                                                                                                                          Matches 119;
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                                                                                70 DDETVRAANLLIKSHTGCVRGVCIDIEKNIPMGGGIGGGSSDAATTIVVINRIMGIGISKR 129
                                                                                                                                                 RWPAPAKLNLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WQCGLSMDSLAEMGLTLGADVPVFVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYABARLTGTG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNÍIVRÁARÍLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL 121
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                                           QNLIYRAAQILRPHAQNPCGLHİKİEKNIPMGAĞLGƏĞSSNAATTLIVLNQLMQCĞLTEE 127
                                                                                                                         RVPSPAKLNLFLHITGRRENGYHELQTIFQLIDLYDWMTFTPISEDEIQIEG-LGEVQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACVFAQFCNKEDAESALEGIKDRWI-VFLAKGLNQSALYKKI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVIFKDPELPRNTPKRSIBTLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
  ELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAEN 189
                                                                                                                                                                                                          Conservative
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43.9*;
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                                                                                                                                                                                                                         Score 589.5; DB (
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Pred. No. 9.7e-60;
                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                             DB 4;
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RESULT 4
US-09-134-001C-3348
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                                                                                                                                                                             Sequence 2, Application US/08596111B Pacent No. 5824873
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LENGTH: 299
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LYNN DOUGETE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND
TITLE OF INVENTION: EPIDERMIDIS FOR
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                               GENERAL INFORMATION:
                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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                 CORRESPONDENCE ADDRESS
                                                   TITLE OF INVENTION:
                                                                                                                                           APPLICANT:
                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                             263
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                                                                                                                                                                                                                                                                                                                                GICACVF 245
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                                                                                                                                                                                                                                                                                             CSGPTVY 269
                                                                                                                                                                                                                                                                                                                                                                   TEEHIVHNEKCKQALENNDYHLLCINGLSINRLEPVSMAMHPDIKKIKDNMLQCGADGALMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAYKAADIMFERFNINEGVTÍSÍDKDIÞVSAGLAGGSADAAATMRGINRIFGLGQSIDAL
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                                                   Schuch, Wolfgang W.
VENTION: DNA, CONSTRUCTS, OVERTION: DERIVED THEREFROM
                                                                                                      Moore, Gloria A.
                                                                                                                                           Grierson,
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White & Durkee
                                                                                                                                               Donald
                                                                                                                                                                                                                                                                                                                                                                                                       LAGDNRNDCSEVVCKLYRPVKDAIDALL-CYAE-ARLT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS
                                                                        CELLS AND
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Houston

P.O. Box 4433

Texas

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; LENGTH: 401
; TYPE: PAT
; ORGANISM: Lycopersicon esculentum
US-09-434-774-10
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09434774A Patent No. 6235514
                                                                                       SEQ ID NO 10
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FILING DATE: 10-APR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9315751.9
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
                                                                                                                                                   FILE REFERENCE: wsur14448
CURRENT APPLICATION NUMBER: US/09/434,774A
CURRENT FILING DATE: 1999-11-04
                                                                                                                                                                                                          APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID WOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USE
                                                                                                            SOFTWARE:
                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 NLIIKALNLYRKKTGTDNYFWIHLDKKVPTGAGLGGGSSNAATTLWAANQESGCVATEKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 18.3%; Score 277; DB 2; Similarity 34.0%; Pred. No. 4.5e-22;
                                                                                                            PatentIn Ver.
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Sequence 16, Application US/09434774A Patent No. 6235514 GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USE
FILS REFREENCE: WEUL14448
CURRENT APPLICATION NUMBER: US/09/434,774A

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09434774A Patent No. 6235514
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 383
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                      197
                                                                                                                188 ENLTRNSAVVIMSDELAGONRNDCSEVVC 216
                                                                                                                                                                                                                                  137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 LMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQW---FVIIKPDCHVNTGEIFSA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 NLIIKALNLYRKKTGTDNYFWIHLDKKVPTGAGLGGGSSNAATTLWAANQFSGCVATEKE 212
                                                                             257 LRIDOTSNINPLT-LLENVISNGVSQSIC
                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                              13 APAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFH-PVDDGRVFLRNPISGVP-EQD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 18.3%;
l Similarity 34.0%;
71; Conservative 43
                                                                                                                                                    LODWSSEIGSDIPPPPSHGAAYCTGRGEIVQDLPPPPPLDLPMVLIKPREACSTAEVYKR 256
                                                                                                                                                                                           IMDIGIRIGADVPVFVFGCSAWGEGVSEDIQAITLP---EQWFVIIKPDCHVNTGEIFSA 187
                                                                                                                                                                                                                                NLIIKALNIYRKKTGSNRFFWIHLDKKVPTGAGI.GGGSSNAATALWAANBINGGLVTENE
                                                                                                                                                                                                                                                                    DLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLARLWGLGLSKRE 130
                                                                                                                                                                                                                                                                                                           SPCKINVFIRITGKREDGFHDLASIFHVISLGDTIKFSLSPSKSKDRLSINVQGVPVDGR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOLDLSSKYDPLS-LLEKISTSGISODVC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENLTRNSAYVIMSDFLAGDNRNDCSEVVC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLTVRAANILKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPCKINVFLRITSKRDDGYHDLASLFHVISLGDKIKFSLSPSKSKDRLSTNVAGVPLDER 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQEWSGEIGSDIPFFFSHGAAYCTGRGEVVQDIPSPIPFDIPMVLIKPQQACSTAEVYKR 272
                                                                                                                                                                                                                                                                                                                                                                                                       18.1%; Score 275; DB 3 33.5%; Pred. No. 7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                      42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 277; DB 3; Length 401;
Pred. No. 4.5e-22;
3; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 383;
                                                                                                                                                                                                                                                                                                                                                                                      91;
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CURRENT FILING DATE: 1999-11-04

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US-09-434-774-16
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Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10
SOPTWARE: PatentIn Ver.
SEQ ID NO 16
LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09434774A Patent No. 6235514
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: wsur14448
CURRENT APPLICATION NUMBER: US/09/434,774A
CURRENT FILING DATE: 1999-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1. SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mentha piperita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 405
                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 91; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                        130 EUMDIGIRIGADVPVFVFGCSAWGEGVSEDIQAITLP---EQWFVIIKPDCHVNTGEIFS 186
                                                                                                                                                                   161 KNLIIKALNUERKKTGTDKHEWIHLDKKVPTGAGLGGGSSNAATALWAANQFSGCIATEK 220
                                                                                                                                                                                                                                                       102 SPCKINVFLRITGKREDGFHDLASLFHVISLGDKIKFSLSPSKFNGSFVTN-VPGVPLDB 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 PAHQPVAQLRQVLQSAGGLGTMMSGSGPSVFTLCREQABAEQVLAIAKEKLNDPDVDFWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 GLSKREIMDIGIRIGADVPVFVFGCSAWGEGVSEDIQAITIPEQ---WFVIIK-PDCHVN 180
                                                                                                                                                                                                                                                                              13 APAKLNIMIRITGRR?DGYHILQTVFQMLDLCDWLTF--HPVDDGRVTLRNPISGVP-EQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 TYLAYRAAQLMINNFPQAHDN-YGGVDITLTKHIPMAAGLAGGSADAAAVLVGEDLLWNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 APAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTF--HPVDDGRVTL-RNPISGVPEQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 DDLTVRAANLL----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGL
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REREDQTSDIDPEVELEKISKGGISQDVCVNDLEPPAFEVVPSEKR-EKQRIAAAGRSQY 339
                                                                                 DIQEWSGEIGSDIPFFFSHGAAYCTGRGEVVEDIPPPVPRDLSMVIMKPQEACPTGEVYK 280
                                                                                                                                                                                                            DDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLYRPVKDAIDALLCYA--EARLTGTGACVFAQFCNKEDAESALEGLKDR------WL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLTRPELEQLAAQLGSDIPFCIGGGTAIATGRGEILD--PLPDGNCFWVVLAKHRSIEVS
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                                      AENITRNSAVVIM------SDFLAGDNRNDCSEVVCKLYRPVKDAIDAL--LCY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPWAYQTYRQKFGKNYLNDDQSQRARRKTIHAGPLLQGIQHRNPGQIASHIHNDLBKVVL
                                                                                                                                                                                                                                                                                                                                      17.3%; Score 263; DB 3; ilarity 30.2%; Pred. No. 1.6e-20; Conservative 50; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.8%; Score 270.5; DB 3; 30.3%; Pred. No. 1.7e-21;
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                                                                                                                                                                                                                                                                                                                                           104;
                                                                                                                                                                                                                                                                                                                                                                               Length 405;
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                                                                                                                                                                                                                                                                                                                                           Indels
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; LENGTH: 99
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-305
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US-09-198-452A-1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT ; ORGANISM: Chlamydia pneumoniae US-09-198-452A-1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                        SEQ ID NO 305
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 1236, Application US/09198452A
Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 305,
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                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILLING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.1
                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Polynuclectides, materials incorporating TITLE OF INVENTION: them and methods for using them.
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                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 LWARBIGSDVPFF 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 IWKSLEIFRRETQIHQPVSWHLMKSIPLQSGLGGGSSNAATALYALNEHFQTHIPITTLQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 APAKLNIMIRITGRRPDGYHLIQIVFQMIDICDWITEHPVDDGRVTLRNPISGVPEQDDI 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 TVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRELM 132
36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05, Application US/09634238
6544772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 11.7%; Score 178; DB 4; Similarity 32.3%; Pred. No. 8.4e-12;
                                                                                                                                                                                                                                                                                                          Holland, Ross
O'Toole, Paul W.
Reid, Julian R.
Coolbear, Timothy
                                                                                                                                                                           FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAKLNIFIKIWGKRFDNFHELTTLYQAIDFGDTLSLK--NSMKDSLSSNVNELLSPSNL 62
                                                                                                                                                                                                                                                                                                                                                                                                                   Lubbers, Mark
Dekker, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Havukkala, Ilkka J.
Bloksberg, Leonard,
                                                                                                                                                                                                                                                                                                                                                                                              Christensson, Anna C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gienn, Matthew
Conservative
                                                                                                                                                                                                                                                         11000.1043U1
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10.6%; Score 160; DB 4;
44.4%; Pred. No. 4.9e-10;
ative 15; Mismatches 30
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                                      Length 99;
    Indels
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: -08-843-521-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31457-6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,521
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5753.
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 783 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                              408
                                                                                                                                                                               108
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                                                                                                                                                                                                                                                                                           43,
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                                                                                                                                                                                                                                                                                                           Similarity
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EGAGLTBIITYA 519
                                                                                                                                            DVEVSSTLADVNRVLGTELSYADVXDVFRRLG-----FGLSG----NADSFTVSVPR
                                                                                                                                                                              SSDAATTLVVLNRLWGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLP- 166
                                                                                                                                                                                                                   GRINIRSESSSRFEKGINVATVNEALDAAASMIAELAGAT-----VRKGIVSAGEIDTS
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                                 ---AIDALLCYA 233
                                                                                                       EQWFVIIKPDCHVNTGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKD-- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LARIGLOVDSDVPYCVYSETA 82
                                                                    RRWDITIEADLEEEIARIYGYDRLPTS---LPKDDGTAGE-----LTVIQKLRRQVRTIA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA
                                                                                                                                                                                                                                                                                       6.0%; Score 91.5; DB 1; Length 783; ilarity 22.4%; Pred. No. 0.38; Conservative 34; Mismatches 76; Indels 3
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linear
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RESULT 14
US-09-134-001C-4141
; Sequence 4141, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
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US-09-012-871-2
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6.0%; Score yi., -
Best Local Similarity 22.4%; Pred. No. 0.38
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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TELEPHONE: 610-270-4478
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ADDRESSEE: SmithKline Seecham Corporation
STREET: 709 Swedeland Road
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TITLE OF INVENTION: No. 6200787el Compounds
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STRANDEDNESS: sir
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REGISTRATION NUMBER: 38.
REFERENCE/DOCKET NUMBER:
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CITY: King of Prussia
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                                                                                                                                           508 EGAGLTBIITYA 519
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                                                                                                                                                                                                                                                                                                      408 DVEVSSTLADVNRVLGTELSYADVXDVFRRLG
                                                                                                                                                                                                                                                                                                                                                                                 354 GRLALRSESSSRFEKGINVATVNBALDAAASMIAELAGAT-----VRKGIVSAGELDTS 407
                                                                                                                                                                                                                                                                                                                                            108 SSDAATTLVVLNRLWGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLP- 166
                                                                                                                                                                                                                                                                                                                                                                                                                       55 GRVTLRNPIS-----GVPEQDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGG 107
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                                                                                                                                                                                   ---AIDALLCYA
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                                                                                                                                                                                                                                                            EQWFVIIKPDCHVNTGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKD-- 224
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No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 91.5; DB
Pred. No. 0.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 783;
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APPLICANT: Lynn Doucette-Stamm et al

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US-09-252-991A-24594
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                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24594
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LENGTH: 315
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRICE PRIOR NUMBER: US 60/074,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24594
LENGTH: 312
TYPER. DET
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Patent No. 6551795
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR PILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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les 30; Conserv
263
                                                                                                    210 QDVPEGLVVALVLAGVGMSRFKAMLVGAASGLVEPLFAVLC-AMLVGLS---
                                                                                                                                                    109 SDAATTIVVINRIWGIGISKREIMDIGIRIGADVPVFVFGCSAWGEGVSEDIQAITIPEQ 168
                                                                                                                                                                                                            155 HPGCEGA-----PLSGGIPPRILLFVTAIVLHMIPEGMAVGVSAGAGLDEAMGLALGIAL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 IPPYELRTEDSRRVLPDTFSHKGAVQNSAI 210
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                                                                                                                                                                                                                                                           50 HPVDDGRVTLRNPIS-GVPEQDDLTVRAANLLKSHTGCVRGVCIDIBKNLPMGGGLGGGS 108
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                                                                                                                                                                                                                                                                                                                44;
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WGLAAAAGAMLFVVTHEIIPESH 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWGLGLSKRELMDLGLRLGA---DVPVFVFG--CSAWGEGVSE--DLQAITLPEQWFVII 173
                                                                                                                                                                                                                                                                                                        5.7%; Score 86; DB 4; Length 312; uilarity 30.8%; Pred. No. 0.39; Conservative 15; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.9%; Score 89; DB 4 ilarity 20.0%; Pred: No. 0.19; Conservative 38; Mismatches
                                               ---FVI---IKPDCH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 315;
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Search completed: January 29, 2004, 15:57:05

Job time : 9.94468 secs

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                               score greater than or equal to the score of the result being and is derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
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length: 2000000000
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Match
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1 MDYAAGWGERWPAPAKLNIM...
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Maximum Match 100%
Listing first 45 summaries
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/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                                                  US-09-934-968-74
US-09-934-868-74
US-09-941-947A-12
US-10-369-493-13766
US-10-369-493-201
US-10-369-493-21079
US-10-369-493-115324
US-10-369-493-15694
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Sequence
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Sequence 74, Appl
Sequence 12, Appl
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            201, App
802, App
21079, A
15324, A
15690, A
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17751, Ap
19184, Ap
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Carcino C	emience oska	3901,	6	10963,	Sequence 358,	e 208, F	e 1236,	10645,	S	e 3024,	89		equence 17829		07,	ወ	14670,	equence 14419	e 11764,	241,		11123,	e 12283,	e 20265,	e 17097,	Sequence 9660, Ap	e 23046,	e 7851,	Sequence 16541, A	Sequence 9956, Ap

ALIGNMENTS

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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 285
TYPE: PRT
ORGANISM: Methylomonas 16a
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                                                                                                                                                            ; FEATURE: OTHER INFORMATION: Amino acid sequences encoded by US-09-934-903-8
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US-09-934-903-8
                                                                                              Query Match
Best Local Sim
Matches 285;
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APPLICANT:
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: September 1, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPIICANT: KOffas, Mattheos
APPIICANT: Odom, J. Martin
APPIICANT: Schenzle, Andreas J.
APPIICANT: No. US2002010259Aiton, Kelley C.
                                                                                                                                                                                                                                                                                                                                                                                            ITLE
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                                                     1 MDYAAGWGERWPAPAKLNLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLR
                                                                                                                 Similarity
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Rouviere, Pierre
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                                                                                             Score 1516; DB 10;
Pred. No. 5.7e-156;
Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/934, CURRENT FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: 60/229, 858 PRIOR FILING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 81 SOFTWARE: Microsoft Office 97 SEQ ID NO 74 LENGTH: 285 TYPE: PRT
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                                                      Sequence 12, Application US/09941947A Publication No. US20030003528A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
APPLICANT: Brzostowicz, Patricia C. APPLICANT: Cheng, Qiong APPLICANT: DiCosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-934-868-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Koffas, Mattheos
APPLICANT: Odom, James M
APPLICANT: Schenzle, Andreas J
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1596 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Methylomonas 16a
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Conservative C
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Pred. No. 5.7e-156;
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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: HERBERSIGN OF MICROBIAL PROTEINS IN ITTLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13766
LENGTH: 279
TYPE: PAT
ORGANISM: Pseudomonas fluorescens
US-10-369-493-13766
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CURRENT FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
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Publication No. US20030233675A1
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APPLICANT:
APPLICANT:
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APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: CARCTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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ORGANISM: Methylomonas
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Miller, Edward S.
Odom, J. Martin
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Query Match Best Local Similarity

42.1%; Score 638; DB 12; 49.6%; Pred. No. 1.2e-60;

Length 279; Indels

0;

Gaps

0

Matches 135;

Conservative

41;

Mismatches

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RESULT 6
US-10-369-493-802
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LENGTH: 279
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 201, Application US/10369493 Publication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                            185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.0%; Score 620; DB 12; al Similarity 48.0%; Pred. No. 1.1e-58; 132; Conservative 36; Mismatches 101;
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                                                                                                                                         FAOFCNKEDAESALEGLKDRWLVFLAKGLNOSALY 279
                                                                                                                                                                                  FIDPELKRNSDIRTLPALLQAPFKNDCEPIARKRFREVEQLLSWLLEYTPSRLTGTGACV 244
                                                                                                                                                                                                                                        FSAENLTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACV
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                                                                                              FGEFESPASARKVLNQAPEWMQGFVARGVNISPLH 279
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Sequence 802, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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                                                                                                                           ; ORGANISM: Xenorhabdus
US-10-369-493-21079
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; ORGANISM: Escherichia coli
US-10-369-493-802
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Soldman, Barry S.
APPLICANT: Chen, Xianfeng
Tifle OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B (118 REFERENCE: 38-10 (52052) B (118 REFERENCE: 38-10 (52052) B (118 REFERENCE: 38-10 (52052) B (118 REFERENCE: 38-10 (52052) B (118 REFERENCE: 38-10 (52052) B (118 REFERENCE: 38-10 (52052) B (118 REFERENCE: 38-10 (52052) B (118 REFERENCE: 38-10 (52052) B (360,039)
FILE SECURIARY DESCRIPTION NUMBER: US 60/360,039
FRIOR FILING DATE: 2002-02-21
FRIOR FILING DATE: 2002-02-21
SECURIARY OF SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECURIARY SECUR
Query Match
Best Local Similarity
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Publication No. US20030233675A1
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Best Local Similarity 47.9%; Pred. No. 3e-58;
Matches 135; Conservative 39; Mismatches 96; Indels 1
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LENGTH: 283
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CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR PILING DATE: 2003-02-28

PRIOR PILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374
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38.6%;
                                                                                                                                                                     nematophilus
Score 584.5; DB 12;
Pred. No. 7.8e-55;
                                    Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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LENGTH: 294
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ITITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
PILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US-60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Server S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-369-493-15324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                              190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLTVRAANLLKSH-----TGCVR-GVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWG 123
ATRAAAEQAMAHLPGNLRAWVVEGAAHSPLLDALD 291
                                                                                                                                                                     TLAELGLRIGADVPVFVRGHNAWAEGVGEKLTPISLPQAAYVLVDPGIHVPTPVLFQSQE 196
                                                                                                                                                                                                                                                          DDLMVRAARALQIHAGTALGAELRVDKRIPAGGGFGGGSSDAATVLVALNALWGLGLPVD 136
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                                         CNKEDAESALEGIKDRWIJVFILAKGINQSALYKKIE 283
                                                                                     LTRDAAPAKTADFASGSLLDNAFEPVLRRREPATEAVFQALSRIGTPRLTGSGSGCFVEF
                                                                                                                            LTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAI-DALLCYAEARLTGTGACVFAQF 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldman, Barry S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Mismatches 102; Indels
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. 9.5e-55;
.ches 105;
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RESULT

38.4%;

Score 582;

DΒ

12;

Length 276;

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FULE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
; ORGANISM: Xanthomonas
US-10-369-493-16082
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US-10-369-493-16082
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US-10-369-493-15690
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16082, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao. Yongwei
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SEQ ID NO 15690
LENGTH: 276
TYPE: PRT
                                                              SEQ ID NO 16082
LENGTH: 276
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Publication No. US20030233675A1
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianieng
TITLE OP INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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CURRENT FILING DATE: 2003-02-28
                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 ATRAAAEQAMAHLPGNLRAWVVEGAAHSPLLDAL 276
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46.0%; Pred. No. 1.4e-54;
tive 41; Mismatches 105;
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US-10-369-493-17751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17751
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17751, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE; 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                 130 ALMHTRLDVAVLAALGLRLGADVPVFVHGCNAWABGVGBCLTPMILPGAAYLLLDPGVCV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
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                                                                                                                                                                                                                                                                                                                        60 RNPISGVEEQDDLTVRAANLLKSHTGCVRGVCIDIEKNLEMGGGLGGGSSDAATTLVVLN 119
                                                                                                                                                                                                                                                                            70 GESVTGVVEADDLVVRAAYLLKYATNVHLGADIFVEKRIPVGGGFGGGSSDAATVLLVLN 129
                                                                                                                                                                                                                                                                                                                                                                       11 VDDGVGW-SAWPAPAKLNLFLQITGRRVDGYHELQTVFRLLDWGDTIHLRVREDGQIHRI 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                               RLWGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHV 179
                                                                                                                                    NTGEIFSAENLTRNSAVVTMSDFLÄGDNRNDCSE-VVCKLYRPVKDÄIDALLCYAEARLT 238
GSGSGCFVEFSTRDEAECALERLPYGLCAWVADGASRSPLLDVLK 294
                                            GTGACVFAQFCNKEDAESALEGIKDRWLVFLAKGINQSALYKKIE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATRAAABQAMAHLPGNLRAWVVEGAAHSPLLDAL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNKEDAESALEGLKDRWLVFLAKGLNOSALYKKL 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRV-TLRNPISGVPEQ 69
                                                                                           PTRELFLDPDLTRDASPATIGDFIAGTAFGNAFEPVLRRRESAVAGALDVLSEVGFARVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTRDAAPAKIADFASGSLLDNAFEPVLRRREPAIEAVFQALSRIGTPRLTGSGSGCFVEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLABIGLRIGADVPVFVRGHNAWAEGVGEKLTPISLPQAAYVLVDPGIHVPTPVLFQSQE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDLMVRAARALQIHAGTALGAELRVDKRIPAGGGFGGGSSDAATVLVALNALWGLGLPVD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 46.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 580.5; DB 12;
Pred. No. 2.3e-54;
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41; Mismatches 105;
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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Satter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/60,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR OF SEQ ID NOS: 47374
SEQ ID NO 9184
LENGTH: 270
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US-10-369-493-9359
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; TYPE: PRT; ORGANISM: Xylella fastidiosa
US-10-369-493-9359
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US-10-369-493-9184
                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH INPROVED PROPERTIES
PILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/360,039
PRIOR APPLICATION NUMBER: US/1374
SEQ ID NO 9359
LEAGHH: 270
TYOPE OF SEQ ID NOS: 47374

SEQ ID NO 9359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9359, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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Publication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 VLAALGLRLGADVPVFVHGCNAMAEGVGECLTPMILPGAAYLLLDPGVCVPTRELFLDPD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNKEDAESALEGLKDRWLVFLAKGLNQSAL 278
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ilarity 47.4%;
Conservative 4
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;; Pred. No. 1.7e-53;
42; Mismatches 98;
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Best Local Similarity

Query Match

Length 270;

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER: OF SEQ ID NOS: 47374
SEQ ID NO 19675
LENGTH: 213
RESULT 15
US-10-369-493-8419
, Sequence 8419, Application US/10369493
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US-10-369-493-19675
; Sequence 19675, Application US/10369493
; Publication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.7%; Score 556; DB 12; Best Local Similarity 51.6%; Pred. No. 6.6e-52; Matches 110; Conservative 34; Mismatches 67;
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                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 WPAPAKLNIMIRITGRRFDGYHLLQTVFQMLBLCDWLTFHFVDDGRVTLRNPISGVPBQD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WPAPAKLNLFLQITGRRVDGYHBLQTVFRLLDWGDTIHLRVRBDGQIHRIGESVTGVVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDLTVRAANILKSHTGCVRGVCIDIEKNLPMGGGIGGGGSSDAATTLVVLNRLMGLGISKR 129
                                                                                                                                                                     LTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPV 222
                                                                                                                                                                                                                                                             ELMDIGIRIGADVPVFVFGCSAWGEGVSEDIQAITIPEQWFVIIKPDCHVNTGEIFSAEN 189
                                                                                                                                                                                                                                                                                                                                                                                                        FPAPAKLNIFILHVIGRREDGYHLLQTVFRFIDHSDRLHFDITHDGVIRHENLIFGLTETD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRDEAECALERLPYGLCAWVADGASRSPL 270
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                                                                                                                                                                                                                     RLMALGLELGADVPVFIYGRNAFABGVGEELHAVDLPSAWYVVLTPPVQISTAAVFTSKE 180
                                                                                                                                                                                                                                                                                                                DLCVRAAKLIRQRFGRESLGVKIHLEKNIPLGGGLGGGSSDAATTLIALNRIWGINWKRE 120
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Pred. No. 1.7e-53;
2; Mismatches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B (TITLE REFERENCE: 38-10(52052)B), 493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-2B
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SEQ ID NO 8419
LENGTH: 233
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Ralstonia metallidurans
                                                                                122
182
                                                                                                                      173 IKPDCHVNTGEIFSAENLTRNSAVVTMSDFLAGDN-----RNDCSEVVCKLYRPVKDAID 227
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                                                                                                                                                                   62 TTLLALINGLWGVNLPREELMRIGLSLGADVPVFVFGQNAFAEGVGEELTPVALPDSWFVV 121
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WIKNYSPHARMIGSGACVFARFEDEQTAQRVMERLPSEWDGRCVKSLSHHPL 233
                                      ALLCYA-EARLTGTGACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSAL 278
                                                                                                                                                                                       TTLVVLARLWGLGLSKRELMDIGLRLGADVPVFVFGCSAWGEGVSSDLQAITLPEQWFVI
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49.1%; Pred. No. 2.4e-49;
tive 35; Mismatches 77;
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Search completed: January 29, Job time: 20.4547 secs 2004, 16:21:17

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Result
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ALIGNMENTS

RESULT 1 F893653 F893653 F893663 F893663 C;Species: Pseudomonas aeruginosa C;Species: Dseudomonas aeruginosa R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener; P.; Hickey, M.J.; B R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener; P.; Hickey, M.J.; B R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener; P.; Hickey, M.J.; B R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener; P.; Hickey, M.J.; B R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener; P.; Hickey, M.J.; B R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener; P.; Hickey, M.J.; B R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener; P.; Hickey, M.J.; B R;Stover; C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener; P.; Hickey, M.J.; B R;Stover; C.G.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; M	SOLIT 1 3063 3063 3063 3063 3063 3063 3063 30
	10 18 d. C

RESULT 2
AH0245
probable 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.-) [imported] C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

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A;Residues: 1-299 <KUR>
A;Cross-references: GB:AL590842;
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                                                                                                                                                                                                                                                                                                    A;Cross-relection:
C;Superfamily: conserved
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A;Residues: 1-283 <POS>
A;Cross-references: EMBL:M77236; NID:g154280; PIDN:AAA27195.1;
A;Cross-references: EMBL:M77236; Drotein HP1443
                                                                                                                                                                                                                                                                                                                                                                                                                   R;Post, D.A.; Hore-Jensen, B.; Switzer, R.L. submitted to the EMBL Data Library, October 1991 A;Description: The prs gene of E. coli and S. typhimurium A;Reference number: S27568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: AH0245
R;Parkhill, J.; Wren
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Best Local Similarity
Matches 140; Conserv
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                                                                                                                   DLTVRAANLL---KSHTGCV---RGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGL 124
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  GLSIDELATLGLTLGADVÞVFVRGHAAFAEGVGEILTÞVNÞÞEKWYLVAHÞGVSIÞTÞVÍ
                                    GLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEI 184
                                                                            NLIVRAARLLMKVASESGRLPAGSGADISIEKRLPMGGGLGGGSSNAATVLVALNHLWQC
                                                                                                                                                           WPSPAKLNLFLYITGQRADGYHTLQTLFQFLDYGDTLHIBPRHDGEIHLLTPVNGVENED
                                                                                                                                                                                                WPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPBQD
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49.8%;
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                                                                                                                                                                                                                                        Score 629; DB 2;
Pred. No. 3.7e-49;
5; Mismatches 96
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Pred. No. 3e-51;
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isopentenyl monophosphate kinase (EC 2.7.1.-) [imported] - Se C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_char
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C;Keywords: phosphotransferase
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th. T.: Connerton, P.; Cronin,
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A; Residues: 1-283 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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Best Local
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                                                                                                                                                                                                                                          NLIVRAARLLMKVASESGRLPAGSGADISIEKRLPMGGGLGGGSSNAATVLVALMHLWQC
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                                                                                                                                                                                                                                                                                                                                                           WPAPAKLNLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQD
FARFDTESCARQVLEQAPE-WLNAFVAKGVNLSPLHREL 282
                                     FAQFCNKEDABSALEGLKDRWL-VFLAKGLNQSALYKKL 282
                                                                                                                 FSAENLTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACV
                                                                                                                                                         GLSIDELATIGITIGADVPVFVRGHAAFAEGVGETLTPVNPPEKWYLVAHPGVSIPTPVI
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                                                                           FKDPQLPRNTPKRSIDTLLKCEFSNDCEVIARKRFREVDAALSWILLEYAPSRLTGTGACV
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Cronin, A.;
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Pred. No. 3.7e-49;
5; Mismatches 96
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Davis,
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Salmonella enterica serov
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, L.; White, N.; Farrar,
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; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Raj Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81875
A;Status: preliminary

R; Parkhill, J.; Achtman, M.; James, ; Holroyd, S.; Jagels, K.; Leather,

K.D.; Bentley, S.; Moule, S.;

S.D.; Churcher, C.; Klee, Mungall, K.; Quail, M.A.;

S.R.; Morel Rajandream,

Z2491

C; Accession:

A81875

A; Status: preliminar A; Molecule type: DNA

hyporhetical protein NMA1092 [imported] - Neisseria meningitidis (strain Z2491 serogroup C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis (C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

A81875

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A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84355.1;
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
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C; Superfamily:
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C;Superfamily:
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A;Residues: 1-283 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 QDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLMGLGLSK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
PVIFKDPELPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
                         GEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTG
                                                                       WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPECHVNT
                                                                                                                              DD£TVRAANLL------KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRL 121
                                                                                                                                                                      QWPSPAKLNLFLYITGQRADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPYEGVEHE
                                                                                                                                                                                                RWPAPAKLMLMLRITGERPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLTRNSAVVTMSDFLAGDN----RNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACV
                                                                                                               DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
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                                                     WQCGLSMDELAEMGLTLGADVPVFVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
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                                                                                                                                                                                                                                           Score 616; DB 2;
Pred. No. 5.5e-48;
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Pred. No. 9.3e-49;
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A;Map position: 26 min
C;Superfamily: conserv
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A; Residues: 1-283 <BLAT>
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                                                                                                                                                                                                Query Match
                                                                                                                                                                                  Local
                        122
                                                     64
                                                                                  70
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                                                                                                                                                                                  Similarity
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A;Cross references: EMBL:U18555; NID:g968925; PIDN:AAC43434.1; PID:g968927
A;Experimental source: strain K-12
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Title: The complete genome sequence in Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64867
A;Status: nucleic acid sequence not shown; translation not shown
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R;Strchmaier, H.; Remler, P.; Renner, W.; Hogenauer, G.
J. Bacteriol. 177, 4488-4500, 1995
A;Title: Expression of genes kdsA and kdsB involved in 3-deoxy-D-manno-octulosonic acid panscriptional level in Escherichia coli K-12.
A;Reference number: I60364; MUID:95362678; PMID:7543480
A;Accession: I83566
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(;Speciles: Escherichia coli
(;Speciles: Escherichia coli
(;Date: 19-Dec:1933 #sequence revision 18-Nov-1994 #text_change
C;Accession: B47706; 183566; E64867; PC1178; 327569
R;Post, D.A.; Hove-Jensen, B.; Switzer, R.L.
J. Gen. Microbiol. 139, 259-266, 1993
A;Title: Characterization of the hemA-prs region of the Escheric A;Reference number: A47706; MUID:93171869; PMID:7679718
A;Accession: B47706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 'M',61-207,'TQAYGRANTKGAPFRRTAVKCRSLGKLLLECAGKCLLRVEAVLQRDVQNRTRSQA'
A;Cross-references: DDBJ:D10264; NID:9216522; PIDN:BAA01106.1; PID:9912433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 121, 127-132, 1992
A;Title: Cloning and characterization of genes involved A;Reference number: JC1381; MUID:93051347; PMID:1427085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000219; GB:U00096; NID:g1787453; PIDN:AAC74292.1; PID:g1787459; A;Experimental source: strain K-12, substrain MG1655
R;Ikemi, M.; Murakami, K.; Hashimoto, M.; Murooka, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-283 <POS
A;Cross-references: EMBL.M77237; NID:g147380; PIDN:AAA24434.1; PID:g147382
A;Experimental source: strain K-12
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                                                           WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNT 181
                                                                                                                                                                            DDLTVRAANLL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTEVVLNRL 121
                                                                                                                                                                                                                                                                                                                              RWPAPAKLNIMIRITGRRPDGYHLIQTVFQMLDLCDWLTFHPVDDGRVTILRNPISGVPEQ 69
                                                                                                                                      DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL 121
                                                                                                                                                                                                                                                                             QWPSPAKLNUFLYITGORADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPVEGVEHE 63
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ilarity 47.9%;
Conservative 3
GADVPVFVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 616; DB 2;
; Pred. No. 5.5e-48;
39; Mismatches 96
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                       conserved hypothetical protein NMB0874 [imported] - Neisseria meningitidis (strain C;Specles: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: B81149
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen
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C; Superfamily: conserved hypothetical protein HP1443
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A;Experimental source: serogroup
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ernolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase, GHMP family VC2182 [imported] - Vibric cholerae (strain N16961 serogroup C;Species: Vibric cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: E82109
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                                                                                                                                                                                                                                                                                                                                        RKDAQAVFAQLSDNVLAFVAQGRNVSPLRKTL
                                                                                                                                                                                                                                                                                                                                                                       KEDAESALEGIKDRWIVFLAKGINQSALYKKI 282
                                                                                                                                                                                                                                                                                                                                                                                                            MRNTPKRDLASLLTTPYENDCEKIVRSLYPEVDKQLSWLLQYAPSRLTGTGSCVFAEFSS 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAEIGLALGADVPVFTRGFAAFAEGVGEELSAVEPEEKWYLVVRPAVSIATKDIFTHPQL
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47.1%; Pred. No. 5.8e-48;
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H.; Dragoi, :
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                                                                                Rappuoli, R.; strain MC58.
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I.; Sellers,
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                                                                                                                                                    Eisen, .
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                            PVIFKDPSLPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
                                                                                                                                                                                                                                                                                                                       Conservative
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A;Residues: 1-283 <STO>
A;Cross-references: GB:AB005174; NID:g12514921; PIDN:AAG56066.1; GSPDB:GN00145;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ychB
C;Superfamily: CTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia c: A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ychB [imported] - Escherichia C;Species: Bscherichia coli C;Dare: 16-Feb-2001 #sequence_revision 16-Feb-2001 C;Accession: F85700
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A;Cross-references: GB:AE002439; GB:AE002098; NID:g7226100; PIDN:AAF41285.1; PID:g722611
A;Experimental source: serogroup B, strain MC58
A;Genetics:
A;Gene: NMB0874
C;Superfamily: conserved hypothetical protein HP1443
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                                                                                         WQCGLSMDELAEMGLTLGADVPVPVPGHAAFAEGVGBILTPVDPPEKWYLVAHPGVSIPT
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                                          GET FSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTG
                                                                                                                                         WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLFEQWFVIIKPDCHVNT
                                                                                                                                                                                                                                          DDLTVRAANLL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRL
                                                                                                                                                                                                                                                                                          QWPSPAKLNLFLYITGQRADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPVEGVEHE
                                                                                                                                                                                                                                                                                                                                            RWPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNP1SGVPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTGTGACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSAL
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                                                                                                                                                                                           DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMXGGLGGGSSNAATVLVALNHL
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                                                                                                                                                                                                                                                                                                                                                                                        40.2%; Score 609; DB 2;
47.5%; Pred. No. 2.4e-47;
tive 39; Mismatches 97
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Pred. No. 6.7e-48
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                                                                                                                                                                                                                                                                                                                                                                                              97;
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imalanta, E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 283
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Potamousis,
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A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Abriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, as-Neto, E.; Docena, C.; Electry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                    C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82532
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MVID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: F82532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000, MUID:95350630; PMID:7542800
A;Accession: A64173
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                                                                                                             A;Residues: 1-298 <SIM>
A;Cross-references: GB:AE004071;
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A; Residues: 1-321 < TIGR>
                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                A;Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNKEDAESALEGIKDRWIVFLAKGINQSALYKKIEQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELADIGIRIGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENNLIYRAAKLIQEKANIQIGANIHIDKIIPMGGGVGGGSSNAATALVSINYIMQANISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPSPAKLNIFIYINGKEPNGYHELQTIFQELDEGDWLDISIREQDWQIVITERIPNIKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHBABAQAVFRQKPBAFFGFVAKGLNVSPLHAMLKQ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACVFAQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFH-PVDDGRVTLRNPISGVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein HP1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:L42023; NID:g1574444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 606.5; DB 2; 47.1%; Pred. No. 4.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45,
                                                                                                                  GB:AE003849; NID:g9107866; PIDN:AAF85442.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: AAC23252.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xylella fastidiosa (strain
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                                                                                                                     GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                          Sequer
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128

AALGEREGADVPVFTRGRAAFAEGVGEKETPVDIPEPWYLVVVPQVEVSTAEIFSDPLET

187

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A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, B.E.; Laigre chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B. A,Authors: Martins, B.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.V.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.U. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki A,Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, R.G.; Salva Jr., W.A.; da Silvaira, R.S.; Vettore, A.L.; Ze M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze A; Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT S49374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein 2 - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 16-Peb-1995 #sequence_revision 01-Feb-1999 #text_change 26-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library,
A;Description: The Escherichia coli
A;Reference number: S49373
A;Accession: S49374
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-221 <TOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Superfamily: conserved hypothetical protein HP1443
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                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                             Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALWHTRLDVAVLAALGLRLGADVPVFVHGCNAWAEGVGECLTPMILPGAAYLLLDPGVCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIWGLGLSKREIMDLGLRIGADVPVFVFGCSAWGBGVSEDLQAITLPEQWFVIIKPDCHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GESVTGVVEADDLVVRAAYLLKYATNVHLGADIFVEKRIPVGGGFGGGSSDAATVLLVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNPISGVPEQDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLN
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                                                                                  LTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKREL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGACVFAQFCNKEDAESALBGLKDRWLVFLAKGLNQSALYKKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTRELFLDPDLTRDASPATIGDFIAGTAFGNAFEPVLRRRESAVAGALDVLSEVGFARVT
    MDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAENLT 191
                                                     LIVRAARGLQBASGSPQGVDIWLDKRLPMGGGIGGGSSDAATTLLALNHLWQLGWDEDRI 127
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                                                                                                                                               PAPAKLNLFLHILGRRDDGYHBLQTLFQFLDHGDBLHFEARQDGQVRLHTEIAGVPHDSN
                                                                                                                                                                                      PAPAKLNIMERITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPBQDD
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46.38;
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                                                                                                                                                                                                                                                          Score 551; DB 2
Pred. No. 3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 580.5; DB 2
Pred. No. 9.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hemN gene encoding
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                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                         71;
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                                                                                                                                                                                                                                                                                Length
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A;Molecule type: DNA
A;Residues: 1-299 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41648.1; PID:g17738989; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ipk [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein ychB [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G84949
                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Yoo, H.; Tao, ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Shigenobu, S.; Watanal
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                  Reference number: AB2577; MUID:21608550; EMID:11743193; Rerelation: AB2654; Status: preliminary
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Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 QYTLKBLSLIGLRIGADVPGFVMGNTAVIEGIGDILYPIVQXEKWYLVVYPCINISTRYM
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Best Local
                                                                  196 IFRRIQNKVNPHLPTPSTIGWATTGWMDFLA-QSRNDLQPPAQALL-PBIGEITGLLSEE 253
                                                                                                                                  136 AIAPEKLKSLALKIGADVPMCLASRPLIARGIGEDIBALTDLPELSMVLANPLKAVSTPE
                                                                                                                                                                   125 GLSKRELMDIGIRIGADVPVFVFGCSAWGEGVSEDLQAIT-LPEQWFVIIKPDCHVNTGE 183
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                       BA---RLTGTGA-C--VFAQFCNKEDAESALBGLKDRW 265
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GATL VRMSGSGATCFGIFHSFDAAKNAETSLRKKRPGW
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35.6%;
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Search completed: January 29, 2004, 15:55:31
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ALIGNMENTS

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ight. It is prod f Bioinformatics stitute. There sons as long as not removed. u reement (See htt b-sib.ch).	-:- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyi-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyi-D-erythritol. D-erythritol:- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth step. Step:- SIMILARITY: BELONGS TO THE ISPE FAMILY.	ក្នុក្សសូមគ	SETRAIN=ATCC 15692 / PAO1; SETRAIN=ATCC 15692 / PAO1; SETRAIN=20437337; PubMed=10984043; MEDLINE=20437337; PubMed=10984043; Stover C.K., Pham XU.T., Erwin A.L., Mizoguchi S.D., Warrener P., Fickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry I., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.KS., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen."; Nature 406:959-964(2000).	E PERAB E PERAB E STANDARD; PRT; 282 AA. ISPE PSEAB OL-NOV-1995 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148) (CMK) (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase). 15PE OR PA4669. Pseudomonas aeruginosa. 13CE-TAXID=287; NCBI_TAXID=287;

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Best Local :
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HAMAP; MF 00061; -; I.

InterPro; IPR006204; GHMP kinase.

InterPro; IPR004424; IspE.

Pfam; PF00288; GHMP kinases; 1.

TIGRPAMS; TIGR00154; ispE; 1.

Transferase; Kinase; Isoprene biosynthesis;
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                                                                                                                                                                                                                     FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By similarity).

CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
                                                                   SIMILARITY: BELONGS TO THE ISPE FAMILY.
                                                                                                                                                  methyl-D-erythritol
PATHWAY: Nonmevalon
               SWISS-PROT
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                                                                                                                                                         terpenoid
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Pred. No. 3.8e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP
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.8e-53;
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                                                                                                                                                      pathway;
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| kinase).
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Best Local S
Matches 140
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28-FEB-2003
28-FEB-2003
28-FEB-2003
                                        SEQUENCE FROM N.A.

STRAIN-CO-92 / Biovar Orientalis;

STRAIN-CO-92 / Biovar Orientalis;

MEDLINE-21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Lieather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL646059; CAD13924.1; -.
HAMAP; MF 00061; -; 1.
InterPro; IPR006204; GHMP kinase.
InterPro; IPR00424; IspB.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMS; TIGR00154; ispB; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR IPK OR YPO2014 OR Y2293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                YERPE
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the Buropean Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                      Enterobacteriaceae;
                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                  SEQUENCE FROM
                                                                                                                                                                                                                                                   NCBI_TaxID=632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNSAVVTMSDF-----LAGDNRNDCSEVVCKLYRPVKDAIDALLCYAE-ARLTGTGAÇVF
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N.A.
Biovar
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                       Yersinia.
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Pred. No. 7.3e-53;
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. kinase).
                                                             plague. *;
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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew < Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Berry R.D.;
QBEARO;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; AH0245; AH0245.

HAMAP; MF_00061; -; 1.

InterPro; IPR006204; GHMP kinase.

InterPro; IPR006424; IspE.

Iffam; PF00288; GHMP kinases; 1.

TIGRFAMs; TIGR00154; ispE; 1.

Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       SHEON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ414151; CAC90828.1; EMBL; AE013832; AAM85852.1;
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J. Bacteriol. 184:4601-4611(2002).

-!- FUNCTION: Catalyzes the phosphorylation of the position group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By
                                                                                                                                                                             ISPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-
erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ISPE
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PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDLTVRAANLLKSHTG----CVRGVCIDIEKNLPMGGGLGGGGSSDAATTLVVLNRLWGLGL
                                                                                                                                                                                                                                                                                                                EFDTESSARQVL-SIAPEWLHGFVARGVNVSPLHR
                                                                                                                                                                                                                                                                                                                                                                                                                             DPELKRNTPIRPLAALISTPYANDCEPIARKRFREVEQALSWILEYAPSRLTGTGACVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AENLTRNSAVVTMSDFLAGDNRNDCSBVVCKLYRPVKDAIDAILCYAEARLTGTGACVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDEQLADIGITIGADVPVFVRGHAAFAEGIGEKLQPAEPVEKWYLVIHPGVNIPTPIIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKREIMDIGIRIGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFS
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                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 A
; 32675 MW;
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Pred. No. 1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
; E86651DA68E0D658 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY.
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                                                                                                                                                                                                                                                                                                                287
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           (EC 2.7.1.148) kinase).
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RA Heidelberg J.F., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,
RA Heidelberg J.F., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,
RA Head T.D., Elsen J.A., Scott J., Beaman M., Brinkac L., Daugherty S.,
RA Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Nueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Meyer T., Saith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
RA Botechnol. 20:1118-1123(2002).

CC -!- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy
CC -!- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy
CC -!- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-
CC --- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-

Tark-Fivil-II-A-T-Fivil-II-1
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/cr send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB015816; AAN56813.1; -.
TIGR; S03836; -.
HAMAP; MF 00061; -; 1.
Piam; PF00288; GHMP kinases; 1.
TIGRPAMs; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
NP_BIND 98
SEQUENCE 284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shewanella oneidensis.
Bacteria; Proteobacteria; Gam
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - i- SIMILARITY: BELONGS TO THE ISPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=70863;
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249
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SQQQALAALAKLPSDMQGFVAKGMNISPLIVRLNR
                                    NKEDAESALEGIKDRWIVFLAKGINQSALYKKIEQ
                                                                                                                                                         ELAAIGLKLGADIEVFIHGFAAFAQGVGERLQAVNPAELWYLVIAPDAHVSTAAVFQDPL
                                                                                                                                                                                                                                                                      DDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR
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                                                                                                                  LTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACVFAQFC
                                                                                                                                                                                                                                                                                                                          WPAPAKLNLFLHINGRRSDGYHELQTLFQFVDCCDQLDFRVTDTPELILHSTMSAVVADS
                                                                                LPRNTPKLGLDTLLSQPWANDCQELVVSKYPQVAKALGWLLEYAPSRWTGTGACVFGEFS
                                                                                                                                                                                                     ELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAEN
                                                                                                                                                                                                                                         DNLILRAAKSI,QQATGFNGGAEIWLDKRLPMGGGLGGGSSDAATTLVALNRLWNTQLSHD
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30721 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 644.5; DB 1;
Pred. No. 5.1e-51;
1; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FE5A22B814242496
                                         284
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Matches 133
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Rhee J.H., Kim :
Choy H.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SBP-2003 (Rel. 42, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-dytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBDFF6;
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Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00288; GHMP kinases; 1.
TIGRFAMS; TIGR00154; ispE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy
group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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PATHWAY: Nonmevalonate terpenoid biosynthesis pathway;
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                                                                                                                                                                     191
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                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                                                                                                                                                                                                                            71 DLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 WPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTEHPVDDGRVTLRNPISGVPEQD
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RSEAESILAQLSDNVSAFVAQGRNISPLKETL
                                                     KEDAESALEGIKDRWLVFLAKGLNQSALYKKL 282
                                                                                                                                                   TRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYABARLTGTGACVFAQFCN
                                                                                                                                                                                                                       LADIGLKLGADVPVFVRGHAAPAEGVGEKLTPAQPEEKWYLVVRPDVHIATVDIFTHPQL
                                                                                                                                                                                                                                                                               LMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAENL 190
                                                                                                             TRNTPKRSLETLLDSEYGNDCEKIVRMIHPKVDKQLSWLLQYAPSRLTGTGSCVFAEFNS
                                                                                                                                                                                                                                                                                                                                    NLIWKAANALQKKTGCTLGANIHLNKILPMGGGIGGGSSNAATALVALNFLWQLGLSDDE
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(Rel. 42, Last sequence up
(Rel. 42, Last annotation
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Pred. No. 8.9e
43; Mismatches
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ISPE VIBPA
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15-SEP-2003 (Rel. 42, Last sequence update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR VP0740.
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MSDLINS-22508454; PubMed=12620739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

Yasunaga T., Honda T., Shinagawa H., Battori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 361:743-749(203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
NP BIND 101
SEQUENCE 295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
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Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio parahaemolyticus.
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CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methy1-D-erythrito1 = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-erythrito1 = ADP + 2-phospho-4-(cytidine 5'-diphospho-4-(cytidine 5'-diphospho-4-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
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132; Conser
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              NKEDAESALEGIKDRWIVFLAKGINQSALYKKIEQ
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                                                                   LTRNTPKRDLETLLNAPSVNDCEKIVRMLYPEVDKQLSWLLQYAPSRLTGTGSCVFAEFS
                                                                                                                        LTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYABARLTGTGACVFAQFC
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Pred. No. 3.2e-50;
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; EF77FF8973E0C76D CRC64;
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Query Match
Best Local S
Matches 140
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EMBL; AE016837; AA068760.1; -.
HAMAP; MF 00061; -; 1
InterPro; IPR006204; GHMP_kinase.
InterPro; IPR00424; ISBE
Pfam; PF00288; GHMP_kinases; 1.
TIGRFAMS; TIGR00154; ispE; 1.
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STEALIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi C718.";
                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as modified and this statement is not removed. It entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: Catalyzes the phosphorylation of the position group of 4-diphosphocytidy1-2C-methy1-D-erythritol (By 2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR IPK OR STY1905 OR T1097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
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28-FEB-2003
                                                                                                                                                                                             Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).

CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ISPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Nonmevalonate terpenoid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration -
en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                             Similarity
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                                                                                                           283 AA;
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                                                                                                           30870 MW;
                             41.5%;
50.2%;
                             Score 629; 1
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  Mismatches
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                                                    Length 283;
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                                                                         BEQUENCE OF 187-283 FROM N.A.

WEDLINE=88257047; PubMed=2838463;

A Hower S.G., Hove-Jensen B., Switzer R.L.;

Beower S.G., Hove-Jensen B., Switzer R.L.;

Synthetase (prsA) in Salmonella typhimurium.*;

J. Bacteriol. 170:3243-3248(1988)

C -!- FUNCTION: CATALYZES THE BHOSPHORYLATION OF THE POSITION 2 H
GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERVTHRITOL (BY
SIMILARITY).

C -!- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-
erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
D-erythritol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

NEDLINE-93171869; PubMed=7679718;

Post D.A., Hove-Jensen B., Switzer R.L.;

"Characterization of the hemA-prs region of the Escherichia (
"Characterization of the hemA-prs identification of two op

Salmonella typhimurium chromosomes: identification of two op

reading frames and implications for prs expression.";

reading frames and implications for prs expression.";
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P30753;
                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21534948; PubMed-11677609;
MCCLElland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P
McClelland M., Sanderson K.E., Spieth J., Dante M., Du F., Hou S., Layman
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney B.,
Ryan B., Sun H., Florea L., Miller W., Stoneking T., Mhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (
4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ESPE OR IPK OR STM1779.
                                                                                                                                                                                                                                                                                                   Mature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                     Ryan B., Sun H., Florea L.
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium
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step.
SIMILARITY: BELONGS TO THE ISPE
CAUTION: Ref.2 sequence differs
frameshift in position 268.
                                                                PATHWAY:
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                                                                Nonmevalonate
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                                                                terpenoid
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                                                              biosynthesis
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                                                                                                -diphospho) -2-C-methyl-D-
5'-diphospho) -2-C-methyl-
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                                                              pathway;
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| kinase).
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Best Local S
Matches 140
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NP BIND 99

CONFLICT 252

SEQUENCE 283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISPE NEIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       StyGene; SG10417; ispE.

HAMA; MF_00061; -; 1.

InterPro; IPR006204; GHMP_kinase.

InterPro; IPR006424; IspE.

Pfam; PF00288; GHMP_kinases; 1.

TIGR00154; ispE; 1.

Transferase, Kinase; Isoprene biosynthesis; ATP-binding;
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EMBL; AE008779; AAL20694.1; --
EMBL; AL9488; --
EMBL; M19488; --
EMBL; M19488; --
PIR; S27732; S27732.
    STRAIN=Z2491 / Serogroup A / Serotype 4A;

MEDLINE=2022556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Klee S.R., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEIMA
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=65699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISPE OR NMA1092.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLTVRAANLL---KSHTGCV---RGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAEFDTESCARQVLEQAPE-WLNAFVAKGVNLSPLHREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAQFCNKEDAESALEGIKDRWI-VFLAKGINQSALYKKI
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50.2%;
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Pred. No. 1
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S -> L (IN REF. 3)
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E33EAF956D12A5BD CRC64;
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AC P5783
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PIR; A81875; A61875;

HAMAP; MF 00061; -; 1.

InterPro; IPR006204; GHMP kinase.

InterPro; IPR004224; ISpE.

Pfam; PF00288; GHMP kinases; 1.

TIGREAMS; TIGRO0154; ispB; 1.
                                                          PASMU STANDARD; PRT; 295 AA.
P5783;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-{cytidine-5'-diphospho}-2-C-methyl-D-erythritol
ISPE OR PM0245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWI
between
Bacteria; Proteobacteria;
Pasteurellaceae; Pasteure
NCBI_TaxID=747;
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Nature 404:502-506(2000).
-i-FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION
GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERVTHRITOL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whitehead S., Spratt B.G., Barrell B.G. Tomplete DNA sequence of a serogroup
                                              Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e Buropean Bioinformatics Institute. There are no restrictions to the property institutions as long as its content is in diffied and this statement is not removed. Usage by and for compatities requires a license agreement (See http://www.isb-sib.ch/ansend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).

CAPALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-crythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE ISPE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                               189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128;
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                                                                                                                                                                                                                                                  FTACQDRNSAYNIYRQVSDLYEAYLAEGLSKHPL
                                                                                                                                                                                                                                                                                                                GLTRNSASSIMETF----ONLOPFRNDMOAVVFKEYPEVWKAYSBLSRYGFALMFGSGACV
                                                                                                                                                                                                                                                                                                                                               NLTRNSAVVTMSDFLAGDN----RNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108
31273 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.2%; Score 624.5;
46.7%; Pred. No. 3.
                                 Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E8A9AB81CCB40BB0
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Pasteurella

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RESULT 11

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15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
Escherichia coli O6.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00061; -; 1.
InterPro; IPR006204; GHMP kinase.
InterPro; IPR004244; IspE.
InterPro; IPR004244; IspE.
InterPro; IPR004244; IspE; 1.
IIGRPAMS; TIGR00154; IspE; 1.
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"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001)
-!- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION 2 HYDROXY GROUP OF 4-DIPHOSPHOCYTIDYL-2C-WETHYL-D-ERYTHRITOL (BY
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NP_BIND 108
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CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
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33064 MW;
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             Gammaproteobacteria;
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9; Mismatches
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XX MEDINE-23388234; PubMed:12471157;
XX MEDINE-23388234; PubMed:12471157;
XX MEDINE-23388234; PubMed:12471157;
XX Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
XX Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
XX Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
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NCBI_TaxID=217992;
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                    (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 41, Last annotation updat
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Pred. No. 8.4e-49;
0; Mismatches 95
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Oshima T., Alba H., Baba T., Fu
Ikemoto K., Inada T., Itoh T.,
Kimura S., Kitagawa M., Makino
Mori H., Motomura K., Nakamura
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Remler P.,
                                                                                                                                                                                                                                                                                                                                                                                     Post D.A., Hove-Jensen B., Switzer R.L.;
"Characterization of the hemA-prs region of the Escherichia coli
Salmonella typhimurium chromosomes: identification of two open
reading frames and implications for prs expression.";
J. Gen. Microbiol. 139:259-266(1993).
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Escherichia coli, and
                                                                                                                                                                                                                              Remler P., Woisetschlaeger M., Strohmaier H.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erythritol."
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MEDLINE=20122571; PubMed=10655484;
Luettgen H., Robdich F., Herz S., Wungsintaweekul J., Hecht S
Schuhr C.A., Fellermeier M., Sagner S., Zenk M.H., Bacher A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaj
Enterobacteriaceae; Escherichia
                                                  MEDLINE=97061202; PubMed=8905232;
                                                                 STRAIN=K12
                                                                                                   Science
                                                                                                                                                                                                                                                                                  Gene 121:127-132(1992).
                                                                                                                                                                                                                                                                                                         Ikemi M., Murakami K., Hashimoto M., Murooka Y.; "Cloning and characterization of genes involved in the biosynthesis of delta-aminolevulinic acid in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93171869; PubMed=7679718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphorylates the
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                                                                                                   complete genome seguence nce 277:1453-1474(1997).
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Baba T., Fujita K., H
, Itoh T., Kajihara M
M., Makino K., Masuda
, Nakamura Y., Nashim
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a K., Hayashi K., Honjo A.,
ihara M., Kanai K., Kashimoto K.,
Masuda S., Miki T., Mizobuchi K.,
Nashimoto H., Nishio Y., Saito N
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Yano M., Horiuchi I., and the "A 718-kb DNA sequence of the "A 718-kb DNA sequence of the 12.7-28.0 DNA Res. 3:137-155 (1996).
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STRAIN-0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
              HAMAP; MF_00061; -; 1.
InterPro; IPR006204; GBMP kinase.
InterPro; IPR006224; ISBB.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMs; TIGR00154; ispB; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                     EMBL; U18555; AAC43434.1; --
EMBL; D18555; AAC43434.1; --
EMBL; AE000219; AAC74292.1; --
EMBL; D90756; BAA36066.1; --
EMBL; AE005338; AAC56066.1; --
EMBL; AP002556; BAB35136.1; --
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EMBL; AF179284; AAF13867.1; --
EMBL; AF116300; AAF29530.1; --
EMBL; AB037116; BAA94247.1; --
EMBL; M77237; AAA24434.1; --
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                                                                                                                                                                                                                   PIR; A90843; A90843.
PIR; B47706; B47706.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M77237; AAA24434.1; ...
EMBL; D10264; BAA01106.1; ALT_FRAME.
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MEDLINE=21074935; PubMed=11206551;
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RES. 8:11-22(2001).

FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION 2 HYDROXY GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL. PHOSPHORYLATES ISOPENTENL HOSPHATE AT LOW RATES. ALSO ACTS ON ISOPENTENOL, AND, MUCH LESS EFFICIENTLY, DIMETHYLALLYL ALCOHOL. DIMETHYLALLYL MONOPHOSPHATE DOES NOT SERVE AS A SUBSTRATE.

MONOPHOSPHATE DOES NOT SERVE AS A SUBSTRATE.

CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-perythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho-4-(cytidine 5'-diphospho-4-(cyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        monophosphate kinase CAUTION: REF.4 SEQUEN
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proteome
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Best Local Sim:
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MEDLINE=20406833; PubMed=10952301;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dichardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

Brmolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

McDonald S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:477-483 (2000).
-!- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POS-
GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERVTHRITOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR VC2182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISPB_VIBCH
                                                                                                                                                                                                                                                                                         SIMILARITY).

CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE ISPE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283
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MEDLINE=2017575; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Tettelin H., Saunders N.J., Heidelberg J.F., Dodson R.J., Eisen J.A., Ketchum K.A., Hood D.W., Pederson J.D., Hickey E.K., Melson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Heischmann R.D., Dougherty Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E Cotton M.D., Utterback T.R., Khouri H., Qin H., Vannathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B
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PIR;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR NMB0874
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InterPro; IPR006204; GHMP kinase
InterPro; IPR004244 IspB.
Pfam; PF00288; GHMP kinases; 1.
PICRFAMS; TIGR00154; ispB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Eacteria; Proteobacteria; Betaproteobacteria;
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Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
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SIMILARITY).
SIMILARITY).
CAPALYTIC ACTIVITY: ATP + 4-(cytidine CAPALYTIC ACTIVITY)
Prythritol = ADP + 2-phospho-4-(cytidine)
                                                                                                  ence 287:1809-1815(2000).

FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION
GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL (BY
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P45271;
  STRAIN=Rd / KW20 / ATCC 51907;
MEDLLNE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.P.
Fleischmann R.D., Bult C.J., Tomb J.-F., Dougherty B.
McKenney K., Sutton G., Fitzhugh W., Fields C.A., (
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelle
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01-NOV-1995 (Rel. 32, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidy1-2-C-methy1-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methy1-D-erythritol
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InterPro; IPR006204; GHMP kinase.
InterPro; IPR004424. ISPE.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMs; TIGR00154; iSPE; 1.
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                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
                                                                                                                                                          SEQUENCE FROM N.A.
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Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
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PATHWAY: Nonmevalonate terpenoid biosynthesis pathway;
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                                                   Clayton R.A., Kirkness
Dougherty B.A., Merrick
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InterPro; IPR006204; GHMP kinase.
InterPro; IPR006224; ISpE.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMs; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q8earo shewanella
Q8dff6 vibrio vuln
Q8dff04 escherichia
Q8df104 escherichia
Q8d246 wiggleswort
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11 WPAPAKLNLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISG-VPEQ 69	Query Match 42.5%; Score 644.5; DB 16; Length 284; Best Local Similarity 49.1%; Pred. No. 1.5e-52; Matches 135; Conservative 41; Mismatches 98; Indels 1; Gaps 1;	GBEARO PRELIMINARY; PRT; 284 AA. (SBEARO; (O1-MAR-2003 (TrEMBLrel. 23, Last sequence update) (O1-MAR-2003 (TrEMBLrel. 23, Last sequence update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation update) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O1-MAR-2003 (TrEMBLrel. 23, Last annotation updates; (O1-MAR-2003) (O

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Best Local Similarity
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Q8FI04;
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QBDFF6;
01-MAR-2003
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Choy H.E.;
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate
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Vibrionaceae; Vibrio.
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Aksoy S.;
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MEDLINE=22388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.,

"Extensive mosaic structure revealed by the complete genome
of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                 flies, Wigglesworthia glossin
Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24494.1; -
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H.,
                                                                                                                                                                                                                                                                                                                                                                                                          Wigglesworthia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
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EMBL; AE016759; AAN80131.1;
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47.9%; Pred. No. 3.1e-50;
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STRAIN-MANA16 / Serotype III;
STRAIN-MEDLINE-22242508; PubMed-12354221;
MEDLINE-22242508; PubMed-12354221;
Glaser P., Rusniok C., Buchrieser C., Ch
Glaser P., Zouine M., Couve E., Lalioui
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Bacteria; Firmicutes; Lactobacillales;
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                                                                                                                                                                                         MDLGLRLGADVPVFVFGCSAWGEGVSEDLQAI-TLPEQWFVIIKPDCHVWTGEIF---SA
                                                                                                                                                                                                                                                                                 TV-RAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLARLWGLGLSKREL
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                                                              KSISRVDIDLLKSAILSSDYQLMVKSMGNSLEDITITKNEVISTIKERMLNSGADVALMT
                                                                                                        ENLTR----
                                                                                                                                                    VAIGFKIGSDVPYCLGGGCSLVLGKGEIVKPLPTLRPCWIVLVKPDFGISTKSIFRDIDC
                                                                                                                                                                                                                                                                                                                         APAKLNIGIDI KGRCDDĞYHELAMIYVSIDLMDYVTISELKEDCIVIDSDSSKMPLNNDN
                                                                                                                                                                                                                                                                                                                                                                  APAKLNIMIRITGRREDGYHLIQTVEQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQDDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFAQPCNKEDAESALEGLKDRWLVFLAKGLNQSALYKKLE 283
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283 AA; 31075 MW; D195DA8A84CC0FE0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 21.9%; Score 332; DB 16; 32.2%; Pred. No. 4.8e-23;
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Last sequence up
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Pred. No. 3.8e-40;
3; Mismatches 98
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ui L., Poyart C., Trieu-Cuot
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Best Local S
Matches 85
QBDS40;
QBDS40;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Putative isopentenyl monophosphate kinase.
IPK OR SMU.1996.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
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4-diphosphocytidyl-2C-methyl-D-erythritol kinase.
ISPE OR SAG0153.
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                                                                                                                                                                           Q8DS40
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TIGR; SAG0133; -.
Kinase; Complete proteome.
SEQUENCE 283 AA; 31047 MW;
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MEDLINE=22222988; PubMed=12200547;
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Hacteria; Firmicutes; Lactobacillales;
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35; Conservative
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Pred. No. 4.8e-23;
i8; Mismatches 107;
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Best Local S
Matches 87
                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-1330 / Biovar 1;

MEDLINE-22247741; PubMed-1227112;

MEDLINE-22247741; PubMed-1227112;

Paulsen I.T., Sehadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Paulsen I.T., Sehadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.B.

Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

"The Brucella suis genome reveals fundamental similarities between
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Q8G2D0;
01-MAR-2003
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                                                        EMBL; AE014350; AAN29340.1; TIGR; BR0394; ~.
                                                                                                        animal and plant pathogens and Proc. Natl. Acad. Sci. U.S.A. 9
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STRAIN=UA159 / ATCC 700610 /
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NCBI_TaxID=1309;
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NCBI_TaxID=29461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
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EMBL; AE015023; AAN59600.1; -.
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(Tramblrel. 23, Last annotation kinase.
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Pred. No. 5.2e-22;
7; Mismatches 102
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                                                                                                        99:13148-13153(2002)
     A9B88FF4157BF513
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01-MAR-2003 (TrEMBLrel.
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Chen Z., Wen Y.;
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STRAIN=ATCC 12228;
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Bacteria; Firmicutes; Bacil
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                                            GTGACVF 245
                                                                                                                                                                            AALGIQIGTDIPFCIYNQTAVCTGRGEQYTFLKRPPSAWVVLAKPNIGISSPDVFKALDL
                                                                                                                                                                                                                                                                   {\tt LAYKAADLMFERFNINEGVTISIDKDIPVSAGLAGGSADAAATMRGLNRLFGLGQSLDAL}
                                                                                                                                                                                                                                                                                                           LTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKREL
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                                                                                       TEEHIVENEKCKQALENNDYHLLCNSLSNRLEPVSMAMHPDIKKIKDNMLQCGADGALMS
                                                                                                                                    TRNSAV-----
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Pred. No. 2.9e-21;
42; Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 302; DB 16;
Pred. No. 3.2e-20;
1; Mismatches 103;
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01-MAR-2003
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01-MAR-2003
01-MAR-2003
01-MAR-2003
                                               MEDLINE=2220067; PubMed=12235376; Takami H., Takaki Y., Uchiyama I.; Takami H. Takaki Y., Uchiyama I.; "Genome sequence of Oceanobacillus iheyensis is Ridge and its unexpected adaptive capabilities
                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (
                                                                                                                                                                                                                                                 Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Oceanobacillus
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                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=HTE831 / DSM 14371 / JCM 11309;
                                                                                                                                                                                                                                NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8EU37
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EMBL; AP005370; BAC08052.1; -.
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MEDLINE=22225144;
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3 311 AA; 33799 MM; 08DF8F2E7726F78A CRC64;
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(TrEMBLrel. 23, Last sequence update)
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monophosphate kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                          iheyensis isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280
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Best Local
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01-JUN-2002 (TrEMBirel. 21, Last sequence update)
01-MAR-2003 (TrEMBirel. 23, Last annotation update)
Putative 4-diphosphocytidyl-2-C-methyl-D-erythri tol kinase
P0003D09.22.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR006204; GHMP kinase.
InterPro; IPR004424; IspE.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMS; TIGR00154; ispB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gramene; Q8S2G0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (FEB-2001) to the EMBL; AP003221; BAB86428.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sasaki T., Matsumoto T., "Oryza sativa (japonica clone: P0003D09.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Screptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinase; Transferase; Complete proteome. SEQUENCE 280 AA; 30957 MW; 4432A4FF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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131 LMDLGLRLGADVPVF----VFGCSAWGEGVSEDLQ---AITLPEQWFVIIKFDCHVNTGE
                                                                              152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TaxID=39947;
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                                                                                                                                                                                                                                                                            ; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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                                                                                                                                                                                                                                                                                                       Similarity
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                                                                           APAKLMLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFH-PVDDGRVTLRNPISGVP-EQD
                                                                                                                        DLTVRAANILKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRE
                                                                                                                                                                              SPCKINVFLRITGKRPDGFHDLASLFHVISLGDTIKFSLSPSKSKDRLSTWVAGVPVDES 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSGSGPTVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNLAYQAAKLFKKTYQIPNGVRIQIBKNIPVSAGLAGGSTDAAAVLRGLNRLFHVNAPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR 129
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                                                                                                                                                                                                                                                                                                                                                                          401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nipponbare;
                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                          43840 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                     Score 274; DB 10;
Pred. No. 2.3e-17;
6; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 280; DB 16;
Pred. No. 3.8e-18;
0; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                          23A259FF4DDCF320 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic DNA,
                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                               81;
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                                                                                                                                                                                                                                                                                                                           Length 401;
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                                 183
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Best Local Similarity
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Q8G6I4;
01-MAR-2003
01-MAR-2003
01-MAR-2003
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01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sanutation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, Cmk,
4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase,
ISPE OR BI0656.
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                                                                Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                   Bifidobacterium longum.
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KAWATABAYASI Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio
Usuda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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   SEQUENCE
                                                                                                                                                Bacteria; Actinobacteria;
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E 315 AA; 32871 MW;
       FROM N.A
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(TremBirel. 23, Last annotation update)
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Pred. No. 9.6e-13;
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                                                                                                                                                Bifidobacteriales;
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QBEZMB PRELIMINAKY;
QBEZMB;
QBEZMB (TremBirel 23, Created)
01-MAR-2003 (TremBirel 23, Last sequence update)
01-MAR-2003 (TremBirel 23, Last annotation update)
4-diphosphotytidyl-2C-methyl-D-erythritol kinase (E
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Schell M.A., Karmirantzou M., Snei B., Vilanova D., E
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley
Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AE011537; AANS1022.1; -. Kinase; Transfersae; Complete proteome.
SEQUENCE 297 AA; 33271 MW; 51AA1F018DAA7872 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002)
EMBL; AE014687; AANZ4478.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pridmore R.D., Arigoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Spirochaetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence of Bifidobacterium longum
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                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                      YDQVSERGDIKNNILYKTFIKARSLFPB-
                                                                                                                                      ISGVPEQDDLT-----VRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATT 114
                                                                                                                                                                                    SPAKINLGLEIPFKRLDGFHEIRSVFLKISWGDDIBIBPASNGVFELFSNNEIILEKRKL
                                                                                                                                                                                                                               APAKLNIMIRITGRREDGYHLLQTVFQMLDLCDWLTFHFVDDGRVTL------RNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAYLGDLASSRSDMRRNHAVLALFAMAQAAEREPDVALTITKRIPVGAGLGGGSADAAAT
                                      LVVLNRL--WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPE-QWFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQAIDAATQAGASHAFVSGSGPSVVAFAADEAAAQRIIEVWRDTAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDAIDAL--LCYABARLTGTGACVFAQFCNKEDAESALEGLKDRWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQWFVIIKPDCHVNTGEIFSAENLTRNSAVVTMSDF----LAGDNRNDCSEVVCKLYRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLAVNRLWEINWPIERLRTIAATLGADMPFCLTGGLAYGTGFGERITDIAPGSRDELALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DLTVRAANLLKSHTGCV------RGVCIDIEKNLPMGGGLGGGSSDAATT
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--LLNFLFSWRPFFTSDEMFVLAAEIGSDVFFFLGEGHAFVTGKGEILEEIEVHHGQGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13,5%;
                                                                                                                                                                                                                                                                               12.9%; Score 196; DB 16; 26.3%; Pred. No. 3.5e-10; tive 53; Mismatches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCEVI/VGAYQSQLSTPZVYHTFDI/VGAAEGDRNHLQAAAISLHPRS
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; Pred. No. 6e-1
44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6e-11
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                                                                                        -LPGVKIHLTKRISPAGGLGGGSTNAAS-
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100
Listing first 45
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                                                                                                   A Geneseq 19Jun03:*

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2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
ב	908	100.0	100.0 157	23	23 ABG61583	High growth methan
N	806	100.0	157	23	AAE22305	Methylomonas 16a 2
ω	806	100.0	157	23	AAU80329	Methylomonas 16a O
4	537	66.6	159	21	AAB11373	E. coli YGBB prote
ហ	537	66.6	159	21	AAB27149	E. coli essential
σ	537	66.6	159	22	AAG63811	2-C-methyl-D-eryth
7	537	66.6	159	24	ABP70685	Escherichia coli 2
œ	534	66.3	158	21	AAB27150	H. influenzae esse
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ABB92639	AAG38717	AAG91445	ABP28012	AAG08216	AAY37797	AAW20173	AAY35167	AAB80182	AAG92667	ABP65843	AAG39032	AAE31686	AAB70488	AAB18226	AAU50581	ABB93990	AAB27153	AAW20628	AAB27154	AAY11013	AAG27633	AAG27448	AAG27449	AAG15275	AAG15276	AAB27152	ABP02539	ABG18263	ABB49155	ABU06061	ABP79612	ABG75686	ABP70688	ABP70687	ABP70686
Herbicidally activ	abidopsis	pro	Streptococcus poly	opsis thal	no acid	ori	Chlamydia pneumoni	Corynebacterium gl	C glutamicum prote	Bifidobacterium lo	Arabidopsis thalia	Rhodococcus erythr	Plasmodium falcipa	Plasmodium falcipa	Propionibacterium	Herbicidally activ	T. pallidum essent	H. pylori cytoplas	H. pylori essentia	H. pylori ORF hp7e	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	11	Synechocystis esse	Human ORFX protein	Novel human diagno	Listeria monocytog	N. meningitidis va	 gonorrhoe 	C-methyl-D-	C-methyl-D-	Å	Ģ.

ALIGNMENTS

ABG61583 standard; Protein; 157 AA.

ABG61583;

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RESULT 1
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XX ABG61586
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WPI; 2002-452200/48
                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000US-229858P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High growth methanotrophic bacterial strain polypeptide #33.
                                                                                                    Koffas M, Odom JM,
                                                                                                                                                                                                                                                                                                                                                                                                                      28-AUG-2001; 2001WO-US26827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methylomonas 16a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200220728-A2.
                                                                                                                                                                                                        DO ( OGUO)
                                                                                                                                                                                                              PONT DE NEMOURS & CO E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                    Schenzle A;
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N-PSDB; ABK83262

New high growth methanotrophic bacterial strain, useful for producing single cell proteins, grows on a Cl carbon substrate, and comprises a functional gene encoding in Embden-Meyerhof carbon pathway

Claim 11; Page 142-143; 157pp; English.

present. The bacterial strain of the invention can be used as a denitrifying agent for the conversion of nitrate or nitrite to nitrous oxide with methane or methanol as a carbon source. It is also used in the production of biomass including proteins, carbohydrates and a wide variety of pigments (particularly for isoprenoid pigments for the purpose of generating animal feeds), in production of terpenoid and carotenoid compounds, useful as pigments and as monomers in polymeric materials and in production of texpolysaccharides at high levels. Sequences ABG61551-ABG61590 represent high growth methanotrophic bacterial strain proteins of the invention. The invention relates to a high growth methanotrophic bacterial strain, which grows on a Cl carbon substrate e.g. methane and methanol, and comprises a functional Embden-Meyerhof carbon flux pathway comprising a gene coding a pyrophosphate dependent phosphofrutokinase enzyme or a 16 RNA. The bacterial strain is useful for the production of single cell protein and for the biotransformation of a nitrogen-containing compound, e.g. ammonia, nitrate, nitrite or nitrogen. It is also useful for the production of a feed product comprising a protein, carbohydrates and a pigment and for reducing oxygen demand, for removing nitrates and nitrites in methane-containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are 168 the

Sequence 157 £,

밁 δ 밁 δ B ঠ Query Match Best Local Similarity Matches 121 157; 61 1 MIRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK HFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD 120 LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157 LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157 HFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD MIRVGMGYÐVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK Conservative 100 .0%; Score 806; DB 23; 0; Mismatches 0 Indels .. Gaps 120 60 60

AAE22305 standard; Protein;

(first entry)

Methylomonas 16a 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase.

RESULT 2
AAE23305
ID AAE2
XX AAE2
AC AAE2
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XX Meth Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase; IspF;

Methylomonas 16a

01-SEP-2000; 2000US-229858P

04-SEP-2001; 2001WO-US27420

01-SEP-2000; 2000US-229907P

DU PONT DE NEMOURS & CO UJ

Brzostowicz PC, curcu Odom JM, Picataggio Cheng Q, , io Dicosimo DJ, Rouviere PB; Koffas Z

2002-351711/38.

Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon

Claim 45; Page 118-119; 156pp; English.

encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. 2C-methyl-d-exythrical 2,4-cyclodiphosphate The method comprises a transformed metabolising carotenoid compounds. suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule control of recularors. (IspF) enzyme used in the invention. carbon in À

Sequence 157 Š

Length

밁 Ś 밁 Ş g Ş Query Match Best Local S Matches 157 121 121 61 61 157; ы Similarity MIRVGMGYDVHRFNDGDHIILGGVKIPVBKGLBAHSDGDVVLHALADAILGAAALGDIGK 60 LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157 HEPOTOPNEKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD MIRVGWGYDVHRPNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK HFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAFKMLFHVPGMRANIAAD LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER Conservative 100.0%; 0 Score 806; DB 23; Pred. No. 1.2e-87; Mismatches Indels ٥. 120 60 120 0

AAU80329 standard; Protein; 157

AAU80329;

15-JUL-2002 (first entry)

Methylomonas 16a ORFS ygbB/ispF protein sequence.

Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive;
keratenoid; pigment; flavour; fragrance; open reading frame 5; ORF5;
ygbB; 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase enzyme; ispF

Methylomonas

WO200220733-A2

14-MAR-2002.

29-AUG-2001; 2001WO-US26852

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RESULT 4
AAB11373
ID AAB1
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Matches 157
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Schenzle A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new nucleic acid molecule encoding an isoprenoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an isoprenoid compound biosynthetic enzyme, and for the microbial production of isoprenoid compounds. The molecules of the invention are also useful for regulating isoprenoid biosynthesis in an organism and for producing recombinant organisms for producing various isoprenoid compounds. The nucleic acid is also useful for feed additive, for the production of keratenoids and their derivatives, isoprenoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 5 (ORP5) ygbB/isp? (2C-methyl-d-erythritol 2s,4-cyclodiphosphate synthase enzyme) protein of the invention, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
      10-APR-1999;
                                                         10-APR-1999;
                                                                                                                                                                          DE19916176-A1
                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                               E. coli YGBB
                                                                                                                                                                                                                                                                                          YJEE; KDTB; YQGF; YGGF; YHBC; YGBP; YGBB; YCHB; antibacterial; treatment; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB11373 standard;
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A, Tomb J;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel Escherichia coli genes (I) encoding proteins (II) designated YQGF, YHBC, YGGJ, YGBP, YCHB, YGBB, YDB and YDTB, and genes (Ia) that encode orthologous gene products (IIa) in other microorganisms and which have antibacterial activity. Recombinant microorganisms in which expression of (I) or (Ia) can be regulated are used to identify compounds that bind to the gene products, particularly in affinity selection assays. (II) and (IIa) are used to identify, or prepare, antibacters and other proteins that bind to the gene products. Substances that bind to the yene protentially useful as antibacterials for treating a wide range of infections in humans and animals. Sequences antisense to (I) and (Ia) can also be used as antibacterials. The specified genes are widely distributed in bacteria but have no close homologs in eukaryotic cells.
                                                                                                                                                                     Bacterial growth; inhibitor; ygbB; yfhC; yacE; ychB; yejD; yrfI; yggJ; yjeB; yiaO; yrdC; yhbC; ygbF; ybeY; gcgB; kdtB; pfs; ycaJ; b1808; yeaA; yagF; b1983; yidD; yceG; yjbC; antibacterial compound; H. influenza; S. pneumoniae; H. pylori; B. burgdorferi; pesticide; M. tuberculosis; antibiotic.
                                                                            19-0CT-2000
                                                                                                            WO200061793-A2
                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                    E. coli essential protein ygbB
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                                                                                                                                                                                                                                                                                                                                                               AAB27149 standard; Protein; 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Essential genes from bacteria, useful in screening for antimicrobial agents, and related proteins, transformants and antisense sequences
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Pred. No. 1.4e-55;
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09-APR-1999; 99EP-0107031. 04-FEB-2000; 2000EP-0102111. 07-APR-2000; 2000WO-EP03135

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RESULT 6
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Best Local S
Matches 107
                                                                                       03-FEB-2000;
07-FEB-2000;
                                                                                                                                                                                                                                              2-C-methyl-D-erythrytol-2,4-cyclodiphosphate synthetase; non-mevalonate pathway; 2-C-methyl-D-erythrytol-2,4-cyclodiphosphate; 2-phospho-4-(cytidine 5'-diphospho) 2-C-methyl-D-erythrytol; CDP-MEZP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to antagonists and inhibitors of 24 bacterial genes and proteins. The proteins are thought to be essential for growth in several species of bacteria (including S. pneumoniae, B. burgdorferi, H. influenza and H. pylori). The proteins and coding sequences shown in the specification can be used to identify antagonists and inhibitors which can be used in disease treatment and pesticides. In particular, they can be used against M. tuberculosis. The present sequence is one of the proteins of the invention.
WPI; 2001-522353/57.
                         Seto
                                                  (SETO/)
                                                                                                                               25-JAN-2001; 2001WO-JP00483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying antibacterial compounds, comprises identifying ar antagonist or inhibitor of the expression of a gene encoding polypeptide essential for bacterial growth or survival -
                                                                                                                                                                                  WO200157223-A1
                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                   2-C-methyl-D-erythrytol-2,4-cyclodiphosphate synthetase
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KUZUYAMA T.
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                       Kuzuyama T.
                                                                                                                                                                                                                                   5'-monophosphate;
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Pred. No. 1.4e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibiotic; isoprenoid synthesis; crystal; (2C-methyl-D-erythritol 2,4-cyclodiphosphate Plasmodium falciparum; ispF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-C-methyl-D-erythrytol-2,4-cyclodiphosphate synthetase. The enzyme is involved in the non-mevalonate pathway. It acts on 2-phospho-4-(cytidine 5'-diphospho) 2-C-methyl-D-erythrytol (CDP-ME2P). to produce 2-C-methyl-D-erythrytol-2,4-cyclodiphosphate and cytidine 5'-monophosphate. The enzyme has a molecular weight of 22 kDa, as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis. The enzyme or gene can be used to increase isoprenoid compound
                                                                         WPI; 2003-167170/16
N-PSDB; ABZ25497.
                                                                                                                                                             Bacher
                                                                                                                                                                                                             (PLAC )
                                                                                                                                                                                                                                                                                                                                                                     13-MAY-2002; 2002WO-EP05238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAH74788
                                                                                                                                                                                                                                                                                         15-MAY-2001; 2001DE-1023597.
25-MAY-2001; 2001US-293875P.
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                                                                                                                                                                                                             MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. BACHER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           co-ordinate data; herbicide; protozoacide; antibacterial;
ric; isoprenoid synthesis; crystal; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                          Hecht S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 AA;
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                                                                                                                                                             Huber
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Pred. No. 1.4e-55;
                                                                                                                                                          Kaiser J,
                                                                                                                                                             Rohdich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthase;
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Novel crystal useful for identifying a potential inhibitor of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, compris

comprises

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RESULT
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Best Local Simi
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a crystal comprising 2C-methyl-p-erythritol 2,4-cyclodiphosphate synthase with or without zinc. The crystal is useful in an inhibitor-screening assay, and identified inhibitors are useful as antibiotics against bacteria or protozoa especially malarial parasite e.g. Plasmodium falciparum, and as herbicides. The inhibitors are also useful for inhibiting the synthesis of isoprenoids. The present sequence is 2C-methyl-p-erythritol 2,4-cyclodiphosphate synthase from Escherichia coli, encoded by the ispF
                                                                                                                                                                    09-APR-1999; 99EP-0107031.
04-FEB-2000; 2000EP-0102111.
                                                                                                                                                                                                          07-APR-2000; 2000WO-EP03135
                                                                                                                                                                                                                                      19-OCT-2000
                                                                                                                                                                                                                                                               WO200061793-A2
                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                          Bacterial growth; inhibitor; ygbB; yfhC; yacB; ychB; yejD; yrff; yggJ; yjeE; yiaO; yrdC; yhbC; ygbP; ybeY; gcpE; kdtB; pfS; ycaJ; b1983; yidD; yceG; yjbC; antibacterial compour the influenza; S. pneumoniae; H. pylori; B. burgdorferi; pesticid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB27150;
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           Disclosure;
                                 Identifying antibacterial compounds, comprises identifying antagonist or inhibitor of the expression of a gene encoding polypeptide essential for bacterial growth or survival
                                                                                         WPI;
                                                                                                                   Loferer
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                                                                                                                                           (GPCB-)
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                                                                                                                                                                                                                                                                                                                                                                                              influenzae essential
                                                                                                                                                                                                                                                                                                                 tuberculosis; antibiotic.
                                                                                       2000-687048/67.
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                                                                                                                 Jacobi A;
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        75pp;
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                                                                                                                                                                                                                                                                                                                                                                                                       Hacterial growth; inhibitor; ygbB; yfhC; yacB; ychB; yejD; yrfI; yggJ; yjeB; yiaO; yrdC; yhbC; ygbP; ybeY; gcpE; kdtB; pfs; ycaJ; b1808; yeaA; yagF; b1983; yidD; yceG; yjbC; antibacterial compound; H. influenza; S. pneumoniae; H. pylori; B. burgdorferi; pesticide; M. tuberculosis; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to antagonists and inhibitors of 24 bacterial genes and proteins. The proteins are thought to be essential for growth in several species of bacteria (including S. pneumoniae, B. burgdorferi, H. influenza and H. pylori). The proteins and coding sequences shown in the specification can be used to identify antagonists and inhibitors which can be used in disease treatment and pesticides. In particular, they can be used against M. tuberculosis. The present sequence is one of the proteins of the invention.
                                                                                                                                                                            WPI;
                                                                                            Disclosure;
                                                                                                                   Identifying antibacterial compounds, comprises identifying an antagonist or inhibitor of the expression of a gene encoding polypeptide essential for bacterial growth or survival.
                                                                                                                      polypeptide
                                                                                                                                                                                                                                                           09-APR-1999;
04-FEB-2000;
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                                                                                                                                                                                                                                 BIOTECH AG
                                                                                         Fig 4;
                                                                                                                                                                                                     Jacobi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                           99EP-0107031.
2000EP-0102111.
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                                                                                          75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 158
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Pred. No. 3.1e-55;
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The present invention relates to antagonists and inhibitors of 24 bacterial genes and proteins. The proteins are thought to be essential for growth in several species of bacteria (including S. pneumoniae, B. burgdorferi, H. influenza and H. pylori). The proteins and coding sequences shown in the specification can be used to identify antagonists and inhibitors which can be used in disease treatment and pesticides. In

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Best Local :
The present invention relates to a crystal comprising 2C-methyl-p-erythritol 2,4-cyclodiphosphate synthase with or without zinc. The crystal is useful an inhibitor-screening assay, and identified inhibitors are useful as antibiotics against bacteria or protozoa especially malarial parasite e.g. plasmodium falciparum, an as herbicides. The inhibitors are also useful for inhibiting the
                                                                                                                                                                                                                                                Novel crystal useful for identifying a potential inhibitor of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, comprises 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein co-ordinate data; herbicide; protozoacide; antibacterial; antibictic; isoprenoid synthesis; crystal; enzyme; 2C-methyl-p-erythritol 2,4-cyclodiphosphate synthase; malaria; Plasmodium falciparum; ispF; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particular, they can be used against M. tuberculosis. The present sequence is one of the proteins of the invention.
                                                                                                                                                                           Example 2; Page -; 214pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2001; 2001DE-1023597.
25-MAY-2001; 2001US-293875P.
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                                                                                                                                                                                                                                                                                                                                                                                                    Bacher A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PLAC )
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Pred. No. 3.1e-
18; Mismatches
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RESULT 11

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Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                          antibiotic; isoprenoid synthesis; crystal; enzyme;
2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase; malaria;
Plasmodium falciparum; ispF; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthesis of isoprenoids. The present sequence is a mutant of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase which was in an example from the invention.

Note: The present sequence is not shown in the specification, derived from the wild-type sequence of Escherichia coli 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (ABP70685)
                                                                                                                                                           Bacher A,
                                                                                                                                                                                                                           15-MAY-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein co-ordinate data; herbicide;
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BACHER A.
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                                                                                                                                                           Hecht S,
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                                                                                                                                                                                                                           2001DE-1023597.
2001US-293875P.
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                                                                                                                                                            Huber
                                                                                                                                                                                                   FOERDERUNG
                                                                                                                                                                                                                                                                                                                                                  "Wild-type His
                                                                                                                                                           æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 531; DB 24;
Pred. No. 7.2e-55;
4; Mismatches 34
                                                                                                                                                            Kaiser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ያ
                                                                                                                                                                                                    WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protozoacide;
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                                                                                                                                                                                                                                                                                                                                                    substituted
                                                                                                                                                              Rohdich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial;
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                                                                                                                                                               Steinbacher
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The present invention relates to a crystal comprising 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase

with

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Example 3; Page -; 214pp;

English

Novel crystal useful for identifying a potential inhibitor 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, compact-methyl-D-erythritol 2,4-cyclodiphosphate synthase proteins.

protein comprises

with

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WPI; 2003-167170/16.

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                         Novel crystal useful for identifying a potential inhibitor of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, comprise 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase protein a
                                                                                                                                                                                                                                                                                                                                                                                  antibiotic; isoprenoid synthesis; crystal; enzyme;
2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase;
Plasmodium falciparum; ispF; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              zinc. The crystal is useful in an inhibitor-screening assay, and identified inhibitors are useful as antibicines against bacteria or protozoa especially malarial parasite e.g. Plasmodium falciparum, and as herbicides. The inhibitors are also useful for inhibiting the synthesis of isoprenoids. The present sequence is a mutant of 2C-methyl-p-erythritol 2.4-cyclodiphosphate synthase which was generated in an example from the invention.
                                                                                                       Bacher A,
                                                                                                                                  (PLAC )
                                                                                                                                                                       15-MAY-2001;
25-MAY-2001;
                                                                                                                                                                                                                                      21-NOV-2002
                                                                                                                                                                                                                                                                 WO200292800-A2
                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                           Protein co-ordinate data; herbicide; protozoacide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase mutant H42S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP70688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP70688 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2C-methyl-D-erythritol
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                                                                                                                                                                                                             13-MAY-2002;
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                                                                                                                                  MAX PLANCK GES
BACHER A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRIGHGFDVSAFGGEGPIIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAALGDIGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPDTDPAFKGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMRVFIABDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
                                                                                                       Hecht S,
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2001US-293875P.
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                                                                                                       Huber R,
                                                                                                                                              FOERDERUNG
                                                                                                                                                                                                                                                                                          "Wild-type His
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Pred. No. 1.6e-54;
4; Mismatches 34
                                                                                                        Kaiser
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                                                                                                                                              WISSENSCHAFTEN
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                                                                                                        Rohdich
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RESULT 13
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ID 75686
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG75686 standard; Protein;
                            WPI; 2003-247867/24
                                                                                                                                                                          18-JUN-2001; 2001US-299058P
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3D molecular structure; protein co-ordinate data; ant:
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                                                                            Louie GV,
                                                                                                                                                                                                                                                                                                                           WO2002102991-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                            Buchanan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   108
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                                                                            SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                         "Featured
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                                                                            Gajiwala KS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a 2C-methyl-D-erythritol 2,4-cyclodiphosphate CC synthase (MSCPS) protein, or a functional MECPS protein subunit, in CC crystalline form. The invention also relates to a computer readable database comprising representation of a compound capable of binding a CC binding pocket of an MECPS protein. The methods are useful for producing CC a compound comprising a 3D molecular structure represented by the CC coordinates contained in a compouter readable database, modulating MECPS protein activity by contacting the MECPS with a compound, identifying an activator or inhibitor of a protein that comprises an MECPS active site or binding pocket, producing a mutant MECPS protein having an altered CC or binding pocket, producing a mutant MECPS protein having an altered CC property relative to an MECPS protein is useful for identifying and CC designing inhibitors and activators of MECPS, for designing and compound CC designing inhibitors and activators of MECPS, for designing format of MECPS corrected biochemical, metabolic or anabolic pathway, or for rational CC drug design to identify and/or design compounds that bind MECPS for corretion of the invention agents. This sequence represents the MECPS
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         N-PSDB; ABZ40582
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                                WPI; 2003-058415/05
                                                                                             Fontana MR,
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                                                                                                                                                                                                                                                                              12-FEB-2002; 2002WO-IB02069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; infection; vaccine; gene therapy
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                                                                                                                                                       (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gonorrhoeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFPDTDPNFKGADSRVLLRHVYGIVKBKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD
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                                                                                          Masignani V,
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Pred. No. 2.1e-53;
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                                                                                            Identifying an antigen for manufacturing a vaccine against meningococcal infection, comprises contacting antibodies with polypeptides, detecting polypeptide-antibody complexes, and it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; antigen; meningitis.
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medicament f
                                                                                                                                                                                                                                                                         Robinson A,
Oliver KJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-2002; 2002WO-GB01399
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DB; ABX09898.
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                                                                                                                                                                                                                                                                                                                                                MICROBIOLOGICAL RES AUTHORITY.
IMPERIAL COLLEGE INNOVATIONS I
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for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 AA;
                                                                                                                                                                                                                                                                         Gorringe
Kroll JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 608; 815pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningococcal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.98;
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                                                                                                                                                                                                                                                                                                 Hudson MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 507; DB 2.
Pred. No. 6e-52;
                                                                                                                                                                                                                                                                              PR;
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                                                                                                                                                                                                                                                                                                 Bracegirdle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogenic bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
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                                                                                                                                                                                                                                                                                                      West DM;
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                                                                                                    identifying
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Claim 37; Page 237-238; 310pp; English

polypeptides as antigens

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cc (a) obtaining antibodies against a commensal bacteria, or an extract (c) polypeptides obtained from an expression library of either a commensal or c polypeptides and (d) (where a polypeptide binds to an antibodies with commensal or c antibodies; and (d) (where a polypeptide binds to an antibody) contacting whether the polypeptides bind to c antibodies; and (d) (where a polypeptide binds to an antibody) c dentifying that polypeptide as an antigen. Also included are: (1) a method of preparing a vaccine composition, comprising identifying c an antigen with the above method, and combining the antigen with a ccarrier; (2) a vaccine composition obtained by the above methods; (d) an antigen identified by the above methods; (d) a polypeptide composition obtained by the above methods; (d) a polypeptide composition of a mucleic acid sequence comprising the composition of comparing the mucleic acid molecule; (d) a method of comparing the mucleic acid molecule; (e) a method of comparing the mucleic acid molecule; (e) a method of comparing the sequence of the first antigen from a pathogenic bacteria, or comparing the sequence of the second antigen from a pathogenic comparing the sequence of the second antigen from a pathogenic comparing the sequence of the first antigen composition of the second antigen and (e) preparing a composition comparing the sequence of the nucleic acid which codes for the first antigen with the sequence of the nucleic acid which codes for the second antigen, and (e) preparing a composition comparish the second antigen, and (f) preparing a composition comparish bacterial infection comprising the first antigen; the method is useful in screening commensal and pathogenic bacterial proteins. The polypeptide antigens by identifying control bacterial proteins that binds to sera raised against commensal composition comparish the methogenic bacterial proteins from the pathogenic bacteria N.
                                                                                                                                                                                                                                                                                                            sequence represents an antigenic protein from the pathogenic bacteria N. meningitidis.
                                                                                                                                                                                                             Sequence
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(a) obtaining antibodies against a commensal bacteria. or a
                                            Local
                                                                                                                                                                                                             160 AA;
                                                                                              Length 160;
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8 Best Loc Matches Query Match 62 FPDTDPNFKGADSRVLLKHVYGIVKEKGYKLVNADVTIIAQAFKMLPHVPGMRANIAADL 121 l Similarity 95; Conserv IRIGQGYDVHQLTEGRKLILGGVEIPFEKGLLGHSDADALLHAVTDALLGAAGLGDIGSH IRVGWGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH Conservative 62.7%; Score 505; DB 24; 60.9%; Pred. No. 9.1e-52; tive 21; Mismatches 40; 40; Indels 0 Gaps ري دي

Search completed: January 29, 2004, 15:49:43 Job time: i5.3511 secs

122 ETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157
|: :|:| | ||||: || ||| || ||: |
124 GIDISCVNIKGKTNEKLGYLGRMEGIEAQAAVLLVR 159

64 FPDTAABFKDADSRVLLRAAYQSVQAQGWQAVNVDTTVIAQKPKLAPHIPQWRANIAADL 123

В